

SEQUENCE LISTING

<110> OULMOUDEN, AHMAD
 JULIEN, RAYMOND
 LAFORET, MARIE-PIERRE
 LEVEZIEL, HUBERT

<120> USE OF SILVER GENE FOR THE AUTHENTICATION OF
 THE RACIAL ORIGIN OF ANIMAL POPULATIONS, AND
 OF THE DERIVATIVE PRODUCTS THEREOF

<130> 0508-1156

<140> 10/565,646
 <141> 2006-03-24

<150> PCT/FR2004/001952
 <151> 2004-07-22

<150> FR/09161
 <151> 2003-07-25

<160> 18

<170> PatentIn version 3.1

<210> 1
 <211> 8146
 <212> DNA
 <213> Bos taurus

<220>
 <221> CDS
 <222> (30)..(104)
 <223> First CDS region

<220>
 <221> CDS
 <222> (2326)..(2435)
 <223> Second CDS region

<220>
 <221> CDS
 <222> (2582)..(2727)
 <223> Third CDS region

<220>
 <221> CDS
 <222> (3804)..(3937)
 <223> Fourth CDS region

<220>
 <221> CDS
 <222> (4315)..(4475)
 <223> Fifth CDS region

<220>
 <221> CDS
 <222> (4733)..(5412)
 <223> Sixth CDS region

<220>
 <221> CDS

<222> (6321)..(6436)
 <223> Seventh CDS region

<220>
 <221> CDS
 <222> (6681)..(6765)
 <223> Eighth CDS region

<220>
 <221> CDS
 <222> (6876)..(7080)
 <223> Ninth CDS region

<220>
 <221> CDS
 <222> (7188)..(7275)
 <223> Tenth CDS region

<220>
 <221> CDS
 <222> (7899)..(8036)
 <223> Eleventh CDS region

<400> 1
 ggtctttggt tgctggaagg aagaacagg atg gat ctg gtg ctg aga aaa tac 53
 Met Asp Leu Val Leu Arg Lys Tyr
 1 5

ctt ctc cat gtg gct ctg atg ggt gtt ctt ctg gct gta ggg acc aca 101
 Leu Leu His Val Ala Leu Met Gly Val Leu Leu Ala Val Gly Thr Thr
 10 15 20

gaa g gtgagtgtgg gatgttgac atgaacaagt gtgaatttgg ggttgcacac 155
 Glu
 25

ctgctctggt ttttctctcc ctaaaatgga agatatcagt agtgcttcag gtgtctccca 215
 cccatttgat ttagtggaga catgggcaac tgagctccct ccccatga agatttgggt 275
 gcatgtgtgt tcaggcactt gggactgaac ctgaaaaaca ccccatctac ctggatgggt 335
 gagagaacag tatgtctccg tggccctaatt ttgagatgc tctgaatagc gagctggaac 395
 atgggtgtcca aggtagtaaa atgagtggaa actcatttag gctttgtctc aggcacttgg 455
 gatagggtat ttaggagata gagaaaagata ggagatagga gaaaggagaa agaggatgg 515
 gtattggata gaagggtaat gaggcacctc atcccccttt tgggatgggc atgggtgaac 575
 acagcccagg cttttgttct ggggctggaa gagacaggca gaagggtctc agctgagcat 635
 cacatgaaa ggcctctggg gattggggcc tctgtacagg agcaaggcgg gtgggtggg 695
 gatggtgaga gggctctggaa tgtcccgtgc tgctctgagg agggaggatt gggagtggag 755
 aaagaatggg gcatcttatg attctcttgt tcttgttggt aggtattcag tgggataatt 815
 ctagatctct ccccaagaga atcaaccagg ttcttggtac atgttagaga tggagtggag 875
 atagtctgtg atgtgcagaa atatctacat tgtacccagc tgcccccttt ctctagatcc 935
 ctggtctcac agactcttg gaaacttctc ttgatctgac ttccctcatt catgtgttga 995
 ttccaagtct tattctttta ctatgttcgt tattgtattc tggaaatatc ctgttcatat 1055
 gtgtccacc caggctctta atatgttgtg ctctactttt ggaatccagat ttttaaaatc 1115
 ataagaagac atttttata agttcatgaa attttgcatg gactgagttt gataattttg 1175
 ttttagtgtg attaacattg tgtttattta agaaaaaaaa atattttttt acagaaacct 1235
 actgaatttg taggggtttta aaataacatg atgtctggga ttgtcttttt aatgcttcag 1295
 ccaaaaaaca aacgaacaac aaaaaataag gatagataaa gcaaatgtga caaaatgctg 1355
 atagtgtgtg gaccttgggg agacacatgc agagccatca catcactttt ttccagacat 1415
 cttcttgggt cagttataat cattttgttt gtccccactc caaattttcta ctgcctcta 1475
 gtccactctc ctactgcttt gccaaagtga tcttctcaaa acacaaatct gatcatattc 1535
 aaaaagcttt tgaagggttaa gttttatggt atatgccata tcatcagta caaaaacaaa 1595
 tcgtctgagg tgccgttgcc tacaggataa agtccaaact cttttgctct gcactccaag 1655
 ccccactct atcttctgg cctactctct catgatgtac atcagccaca ttctagttg 1715
 ctgctcatgg ctttctggct agaagtcttt atgcccagc caactattta ctgtcttctt 1775

SEQCRF05081156

cagtcgacca	gagtgcaatt	tacctgttta	aaatctatca	ttttgttata	cattgtgcat	1835
gtctattatg	gtctcatatta	agcaatgcct	tggattatag	taatttatgt	atatgtctat	1895
ttcatatagt	ttaaactgaa	cccttcaga	accatttctt	tttcatttct	taagtctctt	1955
gcacctgacc	cagtgccctg	tacgtcgtgg	gtattcagta	gattaaaaat	cactttaagg	2015
aacttccctt	gtgtgccaac	aagtggctaa	ggctctgtgc	tcaccaatgc	ggggaccagg	2075
gttcaatctc	aggctcaggga	actagatccc	acaggctaca	actaagagtt	tgcaagccac	2135
aactacctga	cctcacatgc	cacaactaat	cgaagatccc	tcgtgctgca	actaagtcct	2195
agtgtagtta	aatatatctt	tttaatgcac	tttgaatgtg	agaatgaatt	atgtgtcaca	2255
gacactgttg	ttccctgaga	agggagttag	taatgatttg	agggccctca	tagtatatct	2315
tccttttttag ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag						2363
Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Arg Gln						
30 35						
ctc aga att aaa gca tgg aac aga cag ctg tat cca gag tgg aca gaa						2411
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr Pro Glu Trp Thr Glu						
40 45 50						
agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc						2456
Ser Gln Gly Pro Asp Cys Trp Arg						
55 60						
agggaggata tgggtggaat ggggtgggag gggaacgggg ttgaatgtac tttaggaagat						2516
aggggaaggaa aaggcatata gggaggagaa gccaaaggagc taattaatgc agctgccctt						2576
ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg						2625
Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu						
65 70 75						
att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc						2673
Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Pro Pro Lys Ser						
80 85 90						
caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac aac acc atc						2721
Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile						
95 100 105						
atc aat g gtgagtacct ctccgcctcc ttcccaaggt ccagaatccc tggtatcccc						2778
Ile Asn						
110						
aatgagctca aggaatcctc ctctcttttt tttttttttt tttttacaaa ttatatatgt						2838
aacacatatt cactgcagaa aaattagaaa acacagataa accaaaaaga aaaaaaatta						2898
tagttcccca aatggggcac agaagaccga gtggacatag aagttggata gacttggatt						2958
taaaactggtt accagtatgt gaccctggac aagtcactga attgttttgt tcttccattc						3018
ccttatctat agaattggga tgataaacact ttaaaaaggtt cttgtaaggga ttaaaatgtg						3078
ataatataata aagattttag cataatgcct gccctgtgct gtgcttagta ccttagttta						3138
gacgctttgc aaccccatgg actgtagccc accaggctcc tctgtccatg tggattctgc						3198
aggcaagaat actggagttg gtcaccatgc actcctccag gggatctctc caactcaggg						3258
atcgaaacca ggtccttagcc tacagtatta attgatgctg ttatttttcc ttatttccca						3318
ctagctagag cacatcatcc tagacatttt gatacatggc ctaccaattt gtgtccagtg						3378
taagaatata catgtgtgtg ctcatgggct cagtcgtgtc tgactctttg caaccctatg						3438
gactgtgacc cgcgaaagct cctctgccca tgggattgcc cagccaagaa tactggagca						3498
ggttgccatt tcttctccca ggggattctt caacacaggg attgatacct tgtctcctgt						3558
gtttcctgca ttggcagggt tattctttac cactgagcca cctgggaaac cctttaagta						3618
tatacatgca aatcttttat agtttccatt ctcccttcta ccaactccaa taggttatac						3678
caaggagaat gtatttttgt agctaggcag tattcctgga gccctctctt gggagtcagt						3738
ttaaaggttt tgggtgtacg tgagggaatgc cagggaattga gggagactgt ctgtcttctt						3798
ttcag gg agc cag gtg tgg gga gga cag ctg gta tat ccc aca gaa cct						3847
Gly Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro						
115 120 125						

SEQCRF05081156

gat gat acc tgc atc ttc ccc gat ggg gag ccc tgc cct tct ggc cct	3895
Asp Asp Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro	
130 135 140	
cta tct cag aaa aga tgc ttt gtt tat gtc tgg aag acc tgg g	3938
Leu Ser Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp	
145 150 155	
gtaagagttt cccttctctg gcctgtcatt cacacttaaa ttcacttctt cctacctgat	3998
ccccctttctt ttgggtctcat ccttaaatcc ttgtgagtttc cctaactcttc acttccccca	4058
tgactccttc cctctccaca gcacctagtc aactctatta tacttctttc tgggagccct	4118
gtccaatta tagtcccatc ccattggagccc tctcataagg acttttttcc tgcccaacat	4178
atgcaagctt aaactctctg aaataaccat ccttgataca tctcctgacc ttccttctct	4238
ggttcctatc ctaaccctgc ccagctctcc ttggaccagt aacccccctc cctactcttc	4298
tttccaaaaa cctcag ac caa tac tgg caa gtt ctg ggg ggc cca gtg tct	4349
Asp Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser	
160 165	
gga ctg agc atc ggg aca gac aag gca atg ctg ggc aca tat aac atg	4397
Gly Leu Ser Ile Gly Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met	
170 175 180	
gaa gtg act gtc tac cac cgc cgg ggg tcc cag agc tat gtg ccc ctc	4445
Glu Val Thr Val Tyr His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu	
185 190 195 200	
gct cac tcc agt tca gcc ttc acc att act g gtaaggactg aggaggggac	4496
Ala His Ser Ser Ser Ala Phe Thr Ile Thr	
205 210	
aaggccagtt gcagggcagg agaaggtggg gaggtctggc tggacaggaa aggggaaaga	4556
ggaaatgggt tgtaacctta caggggcaga accaggaaga tgtgggcaga gggatgtggg	4616
gcttggagcc cgtgaagggc caggcagctt gggttgggtg aaaaatatgg ctgtgaaaga	4676
agaagctgac agaagaaga acttatggtt ctactttct ctgactccaa tccag ac	4734
Asp	
cag gtg ccc ttc tct gtg agt gtg tct cag ctg cag gcc ttg gat gga	4782
Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala Leu Asp Gly	
215 220 225	
agg aac aag cgc ttc ctg aga aag cag cct ctg acc ttt gcc ctc cag	4830
Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe Ala Leu Gln	
230 235 240	
ctc cat gat ccc agt ggc tat ttg gct ggg gct gac ctt tcc tac acc	4878
Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu Ser Tyr Thr	
245 250 255	
tgg gac ttt ggt gac agt aca ggg acc ctg atc tct cgg gca ctc acg	4926
Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg Ala Leu Thr	
260 265 270 275	
gtc act cac act tac cta gag tct ggc cca gtc act gca cag gtg gtg	4974
Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala Gln Val Val	
280 285 290	
ctg cag gct gcc att cct ctc acc tcc tgt ggc tcc tct cca gtt cca	5022
Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser Pro Val Pro	

295	300	305	
ggc act aca gat agg cat gtg aca act gca gag gct cct gga acc aca Gly Thr Thr Asp Arg His Val Thr Ala Glu Ala Pro Gly Thr Thr	310 315	320	5070
gct ggc caa gtg cct act aca gaa gtc atg ggc acc aca cct ggc cag Ala Gly Gln Val Pro Thr Thr Glu Val Met Gly Thr Pro Gly Gln	325 330	335	5118
gtg cca act gca gag gcc cct ggc acc aca gtt ggg tgg gtg cca acc Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp Val Pro Thr	340 345	350 355	5166
aca gag gat gta ggt acc aca cct gag cag gtg gca acc tcc aaa gtc Thr Glu Asp Val Gly Thr Thr Pro Glu Val Ala Thr Ser Lys Val	360	365 370	5214
tta agt aca aca cca gtg gag atg cca act gca aaa gct aca ggt agg Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala Thr Gly Arg	375 380	385	5262
aca cct gaa gtg tca act aca gag ccc tct gga acc aca gtt aca cag Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr Val Thr Gln	390 395	400	5310
gga aca act cca gag ctg gtg gag acc aca gct gga gag gtg tcc act Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu Val Ser Thr	405 410	415	5358
cct gag cct gcg ggt tca aat act agc tca ttc atg cct aca gaa ggt Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro Thr Glu Gly	420 425	430 435	5406
act gca g gtaagggggc caccatgaat gagttcatag aggtggggca tttgtcacag Thr Ala			5463
ctctgaagac ctgaaagaat tgctcaggac ccagatgtta ctcaatcctt agcttagcag tggagtcctc tcagaatctt cactgggttt aaaacccctt aagtcctctt taatggcaca gaatagatct agagttcagg aaaccagggt ctctccttag gccaggggta gagagcttat tctctcttcc tgaagagaag ttccaggaagc agtggtgtgat catttggttg tgggtgctcag tcattgtctga ctctttgtga cctcatggac tatggcccac caggctctctc tgtccataga atttctccagg caagaacact ggagtggttg gccatttctt tctccagggg attttccctc cccagggatt aaaccgaact tggcagggtg attctttacc cgagccacct agaaaagtcct atgtgatcat tagataaatc ttatacctca ttttctgatt aagtgtaaac acagaaatct ttctgacacc acttcccacc cctggattcc catcccctaa taggtttacc tgggaattgtg tgaggaaatc taaaaagggg gaagtggatc agtgacacta tgacttaaca catgtcaaat gtctgaccac ggacctggca cagtgtaggg tgtgataaac atttgggatg tctaaaaattc tgactctaac cctgtgactc tggggcagtc atttctcttg ggcccttctt tatcttaaaa aatgagagtt tccagctctt gctgattct aagcctggat ccagtagctc tgactctacc tggaaaaaatg ctgtgtgggc ctgttttcag gttagtcatc tgccttttga ctttgccctc			5523 5583 5643 5703 5763 5823 5883 5943 6003 6063 6123 6183 6243 6303
ttaatcctct cctccag gc tcc ctg agt ccc ctg ccg gat gac act gcc Gly Ser Leu Ser Pro Leu Pro Asp Thr Ala	440	445	6352
acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr	450 455	460	6400
cgc tat ggc tcc ttt tcc ctc acc ctg gac att gtc c gtagtcttg Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val	470	475	6447

SEQRF05081156

cctacattgt	ccgtaagctg	gtggaggagg	gcgtgtgctg	cttaggggtg	cccagtgga	6507			
gcacacctg	gaaggaatta	ctcacctgga	caaggagaat	accagatcc	caggggttc	6567			
atatgaaggc	agaatgggat	tagggaggca	gcccgaggac	cttctcgcc	atgggccttg	6627			
ggggaggata	agtagaggag	tctcagactt	aaaaaaaaat	tgcaactttg	cag ag	6682			
					Gln				
ggt att	gag agt	gct gag	atc cta	cag gct	gtg tca	tcc agt	gaa gga	6730	
Gly Ile	Glu Ser	Ala Glu	Ile Leu	Gln Ala	Val Ser	Ser Ser	Glu Gly		
	480		485		490				
gat gca	ttt gag	ctg act	gtg tct	tgc caa	ggc gg	gtgagtgtcc		6775	
Asp Ala	Phe Glu	Leu Thr	Val Ser	Cys Gln	Gly Gly				
	495		500		505				
cacggttgcc	ctgagaactc	ctgggggtgac	tgctgtctg	ttctctggtg	tctagtgtcc			6835	
cttcccagat	tccttgacgt	aagctgacat	ctctcccag	g cta	ccc aag	gaa gcc		6890	
					Leu Pro	Lys Glu	Ala		
							510		
tgc atg	gac atc	tca tcg	cca ggg	tgt cag	ctg cct	gcc cag	cgg ctg	6938	
Cys Met	Asp Ile	Ser Ser	Pro Gly	Cys Gln	Leu Pro	Ala Gln	Arg Leu		
	515			520			525		
tgt cag	cct gtg	ccc ccc	agc cca	gcc tgc	cag ctg	gtt ttg	cac cag	6986	
Cys Gln	Pro Val	Pro Pro	Ser Pro	Ala Cys	Gln Leu	Val Leu	His Gln		
	530			535		540			
gta ctg	aag ggt	ggc tca	ggg acc	tac tgc	ctc aat	gtg tct	ttg gct	7034	
Val Leu	Lys Gly	Gly Ser	Gly Thr	Tyr Cys	Leu Asn	Val Ser	Leu Ala		
	545		550		555				
gat gcc	aat agc	ctg gcg	atg gtc	agc acc	cag ctt	gtc atg	cct g	7080	
Asp Ala	Asn Ser	Leu Ala	Met Val	Ser Thr	Gln Leu	Val Met	Pro		
	560		565		570				
gtaggtagt	ggacaagagg	taggatgaag	acacggggag	atggtagagg	ttacctacta			7140	
gaggaagcag	acactgaatg	cagccgtatc	tgggattcca	cccatag gg	caa gaa			7195	
					Gly Gln	Glu			
						575			
gca ggc	ctc agg	cag gct	cct ctg	ttc gtg	ggc atc	ttg ctg	gtg cta	7243	
Ala Gly	Leu Arg	Gln Ala	Pro Leu	Phe Val	Gly Ile	Leu Leu	Val Leu		
	580			585		590			
aca gct	ttg ttg	ctt gca	tct ctg	ata tac	ag gtg	gatgatccc	cgccatcctg	7295	
Thr Ala	Leu Leu	Leu Ala	Ser Leu	Ile Tyr	Arg				
	595		600						
ctccactcc	tttaccctt	attaccacca	ccactcttcc	tcatgggaag	aagaaaccac			7355	
caaccccttt	gggaaagtgt	agagtccaag	aaagagccca	gacttgggaag	ttcaacaggt			7415	
ctaggtctgca	gtcttgcctg	tgggaccctg	gggaagtcca	ttaaccccttc	tgagccactg			7475	
aaaagttagga	aacataatac	ctgtctctgtg	gggctgtttt	cagggctcta	gacaatgtga			7535	
gtaaaaacac	tggttctgaa	acaaaagtgg	aataaatgat	gattctcaatg	actgttgtta			7595	
tgaataatat	caacagtggg	gaagaactca	gtgaactgag	ttctccacct	gccagaaaag			7655	
caaatcccta	ggcctggagg	gctgaggtcc	tcaaagcagg	gaagcctgta	gggtgagagg			7715	
gaaatggtca	gagcttacc	taaacataag	agaggataaa	ccctgttggt	gagaagagga			7775	
gggagcagg	atcaagacca	agtcaccctg	ggttatgggt	tagctctttt	tttttagaga			7835	
agcacaaga	ggttgcatt	gaccaccact	aaccagtatc	cctgcttttc	ttccaatatc			7895	
ag g	cga aga	ctt atg	aag caa	ggc tca	gca gtc	ccc ctt	ccc cag	ctg	7943

SEQCRF05081156

Arg Arg Leu Met Lys Gln Gly Ser Ala Val Pro Leu Pro Gln Leu
605 610 615

cca cac ggt aga acc cag tgg cta cgt ctg ccc tgg gtc ttc cgc tct 7991
Pro His Gly Arg Thr Gln Trp Leu Arg Leu Pro Trp Val Phe Arg Ser
620 625 630

tgc ccc att ggt gag agc aaa ccc ctc ctc agt gga cag cag gtc 8036
Cys Pro Ile Gly Glu Ser Lys Pro Leu Leu Ser Gly Gln Gln Val
635 640 645

tgagtgtctt tatgtgaagt catgatttac ccagggtggac agcaaggcct gtctttttctc 8096
tggctcttcc tcagagacta ccattgcctg aaataaagac tcagaacttg 8146

<210> 2
<211> 649
<212> PRT
<213> Bos taurus

<400> 2
Met Asp Leu Val Leu Arg Lys Tyr Leu Leu His Val Ala Leu Met Gly
1 5 10 15

Val Leu Leu Ala Val Gly Thr Thr Glu Gly Pro Arg Asp Arg Asp Trp
20 25 30

Leu Gly Val Ser Arg Gln Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu
35 40 45

Tyr Pro Glu Trp Thr Glu Ser Gln Gly Pro Asp Cys Trp Arg Gly Gly
50 55 60

His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
65 70 75 80

Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser Gln Lys Val
85 90 95

Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly
100 105 110

Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro Asp Asp
115 120 125

Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro Leu Ser
130 135 140

Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp Asp Gln Tyr Trp
145 150 155 160

Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Asp Lys
165 170 175

Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr His Arg Arg
180 185 190

Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr
195 200 205

Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala
210 215 220

Leu Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe
Page 7

225											SEQCRF05081156										240
Ala	Leu	Gln	Leu	His	245	Asp	Pro	Ser	Gly	Tyr	250	Leu	Ala	Gly	Ala	Asp	255	Leu	240		
Ser	Tyr	Thr	Trp	260	Asp	Phe	Gly	Asp	Ser	265	Thr	Gly	Thr	Leu	Ile	270	Ser	Arg			
Ala	Leu	Thr	Val	275	Thr	His	Thr	Tyr	280	Leu	Glu	Ser	Gly	Pro	285	Val	Thr	Ala			
Gln	Val	Val	Leu	Gln	Ala	295	Ile	Pro	Leu	Thr	Ser	300	Cys	Gly	Ser	Ser					
Pro	305	Val	Pro	Gly	Thr	310	Asp	Arg	His	Val	315	Thr	Ala	Glu	Ala	Pro	320				
Gly	Thr	Thr	Ala	Gly	Gln	325	Val	Pro	Thr	Thr	330	Glu	Val	Met	Gly	Thr	Thr				
Pro	Gly	Gln	Val	340	Pro	Thr	Ala	Glu	Ala	345	Pro	Gly	Thr	Thr	Val	350	Gly	Trp			
Val	Pro	Thr	Thr	Glu	Asp	Val	Gly	Thr	Thr	Pro	Glu	Gln	Val	Ala	Thr						
Ser	Lys	370	Val	Leu	Ser	Thr	375	Pro	Val	Glu	Met	Pro	380	Thr	Ala	Lys	Ala				
Thr	385	Gly	Arg	Thr	Pro	Glu	390	Val	Ser	Thr	Thr	Glu	395	Pro	Ser	Gly	Thr	Thr	400		
Val	Thr	Gln	Gly	Thr	405	Thr	Pro	Glu	Leu	Val	410	Glu	Thr	Thr	Ala	Gly	Glu				
Val	Ser	Thr	Pro	Glu	Pro	Ala	Gly	Ser	Asn	Thr	Ser	Ser	Phe	Met	Pro						
Thr	Glu	Gly	Thr	Ala	Gly	Ser	Leu	440	Ser	Pro	Leu	Pro	Asp	445	Asp	Thr	Ala				
Thr	Leu	Val	Leu	Glu	Lys	Arg	455	Gln	Ala	Pro	Leu	Asp	460	Cys	Val	Leu	Tyr				
Arg	465	Tyr	Gly	Ser	Phe	Ser	470	Leu	Thr	Leu	Asp	Ile	475	Val	Gln	Gly	Ile	Glu	480		
Ser	Ala	Glu	Ile	Leu	Gln	Ala	Val	Ser	Ser	490	Ser	Glu	Gly	Asp	Ala	495	Phe				
Glu	Leu	Thr	Val	500	Ser	Cys	Gln	Gly	Gly	505	Leu	Pro	Lys	Glu	Ala	510	Cys	Met			
Asp	Ile	Ser	515	Ser	Pro	Gly	Cys	Gln	520	Leu	Pro	Ala	Gln	Arg	525	Leu	Cys	Gln			
Pro	Val	Pro	Pro	Ser	Pro	Ala	535	Cys	Gln	Leu	Val	Leu	540	His	Gln	Val	Leu				
Lys	545	Gly	Gly	Ser	Gly	Thr	550	Tyr	Cys	Leu	Asn	Val	555	Ser	Leu	Ala	Asp	Ala	560		

SEQCRF05081156

Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly Gln Glu
565 570 575
Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu
580 585 590
Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys
595 600 605
Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg Thr Gln
610 615 620
Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser
625 630 635 640
Lys Pro Leu Leu Ser Gly Gln Gln Val
645

<210> 3
<211> 8146
<212> DNA
<213> Bos taurus

<220>
<221> CDS
<222> (30)..(104)
<223> First CDS region

<220>
<221> CDS
<222> (2326)..(2435)
<223> Second CDS region

<220>
<221> CDS
<222> (2582)..(2727)
<223> Third CDS region

<220>
<221> CDS
<222> (3804)..(3937)
<223> Fourth CDS region

<220>
<221> CDS
<222> (4314)..(4475)
<223> Fifth CDS region

<220>
<221> CDS
<222> (4732)..(5412)
<223> Sixth CDS region

<220>
<221> CDS
<222> (6321)..(6436)
<223> Seventh CDS region

<220>
<221> CDS
<222> (6681)..(6765)
<223> Eighth CDS region

SEQCRF05081156

```

<220>
<221> CDS
<222> (6876)..(7079)
<223> Ninth CDS region

<220>
<221> CDS
<222> (7188)..(7275)
<223> Tenth CDS region

<220>
<221> CDS
<222> (7899)..(8036)
<223> Eleventh CDS region

<400> 3
ggctcttgggt tgctggaagg aagaacagg atg gat ctg gtg ctg aga aaa tac 53
Met Asp Leu Val Leu Arg Lys Tyr
1 5

ctt ctc cat gtg gct ctg atg ggt gtt ctt ctg gct gta agg acc aca 101
Leu Leu His Val Ala Leu Met Gly Val Leu Leu Val Arg Thr Thr
10 15 20

gaa g gtgagtgtg gatgttggac atgaacaagt gtgaatttgg ggtgtcacac 155
Glu
25

ctgctctgggt ttttctctcc ctaaaatgga agatatcagt agtgcttcag gtgtctccca 215
ccatttggat ttagtggaga catgggcaac tgagctccct ccccatatga agatttgggt 275
gcatgtgtgt tcaggcactt gggactgaa ctgaaaaaca ccccatctac ctggatgggt 335
gagagaaacag tatgtctcgg tggccttaat ttgagatgc tctgaatagt gagctggaac 395
atgggttgcca aggtagttaa atgagtggaa actcatttag gctttgtctc aggcacttgg 455
gatagggtat ttaggagata gagaagata ggagatagga gaaaggagaa agaggatgtg 515
gtattggata gaagggtaat gaggcacctc atccctctt tgggatgggc atgggtgaac 575
acagcccagg cttttgttct ggggctggaa gagacaggca gaagggtctc agctgagcat 635
cacatgaaag ggcctcgggg gattggggcc tcgtgacagg agcaaggcgg gtggggtggg 695
gatgggtgaga gggctcggaa tgctccgtgc tgctctgagg agggaggagt gggagtggag 755
aaagaatggg gcatcttatg attctcttgt tcttgtgggt aggtattcag tgggaatttt 815
ctagatctct ccccaagaga atcaaccagg ttctgtgtac atgttagaga tggagtggag 875
atagtctgtg atgtgcagaa atatctacat tgtaccccag tgcccccttt ccttagatcc 935
ctggctctcac agacttcttg gaacttctcc ttgactctgac ttccctcatt catggtgtca 995
tttcaagctc tattctttta ctatgttcgt tattgtattc tggaaatcct ctgttcatat 1055
gtgtccaccc aaggctctta atatgttgtg cttacttttt ggatccagat ttttaaaatc 1115
ataagaagac atttttatat agttcatgaa attttgcag gactgagttt gataattttg 1175
tttagtgttg attaacattg tgtttattta agaaaaaaa atattttttt acagaaacctt 1235
actgaatttg tagggtttta aaataacatg atgtctggga ttgtcttttg aatgcttcag 1295
ccaaaaaaca aacgaacaac aaaaaataag agatagataa gcaaatgtga caaaatgctg 1355
atagtgtgtg gaccttgggg agacacatgc agagccatca catcactttt ttccagacat 1415
ctttcttgtg cagttataat cattttgttt gtccccactc ccaatttcta ctgtccctta 1475
gtccatctct ctcactgctt gccaaaagta tccttctaaa acacaaattc gatcatattc 1535
aaaaagcttt tgaagggtaa gttttatggt atatgccata tatcagtaca acaaaaacaa 1595
tcgtctgagg tgccgttgcc tcacaggataa agtccaaact cctttgcctg gcactccaag 1655
cccccaactt atcttcttgg cctcatctct catgatgtac atcagccaca ttgctagtgt 1715
ctgctcatgg ccttctgcct aagaatgctt atgccccagc caactattta ctgtcttctt 1775
cagtgaccac gagtcaattt tacctgttta aaatctatca ttttgttata cattgtgcat 1835
gtctattatg gctcatatta agcaatgcct tggattatag taattttatg atatgtctat 1895
ttcatatact ttaactctgaa ccccttcaga accatttctt ttctatttct taagtctctt 1955
gcacatagcc cagtcctggg tacgtctgtg gtattcagta gattaaaaatg cactttaaag 2015
aacttccctt gttgtccatc aagtggtctaa ggctctgtgc tcccaatgca gggaccagg 2075
gttcaatctt aggtcaggga actagatccc acaggtcaca actaagagt ttgcaaggcc 2135
aactacctga cctcacatgc cacaactaat cgaagatccc tcgtgtctga actaagctct 2195

```

SEQCRF05081156

agtgacagtt	aatatat	ttttatgcac	tttgaatgtg	agaatgaatg	atgtgtcac	2255
gacactgttg	tcccctgaga	agggagtgag	taatgatttg	agggccctca	tagtatact	2315
tcctttttag	ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag					2363
	Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Arg Gln	30			35	
ctc aga att aaa gca tgg aac aga cag ctg tat cca gag tgg aca gaa						2411
Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr	40	45	50			
agc cag ggg cct gac tgc tgg aga g gtaggaactt ggcaatttcc						2456
Ser Gln Gly Pro Asp Cys Trp Arg	55	60				
agggaggata tgggtggaat ggggtgggag gggaacgggg ttgaatgtac ttaggaagat						2516
aggggaaggaa aaggcataca gggaggagaa gccaaaggagc taattaatgc agctgccctt						2576
ttcag gt ggc cac ata tcc ctg aag gtc agc aat gat ggg cct aca ctg						2625
Gly Gly His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu	65	70	75			
att ggg gca aat gct tcc ttc tct att gcc ttg cac ttt cct aaa agc						2673
Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser	80	85	90			
caa aag gtg ctg cca gat ggg cag gtc atc tgg gcc aac aac acc atc						2721
Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile	95	100	105			
atc aat g gtgagtacct ctccgcctcc ttcccaaggt ccagaatccc tggatatcccc						2778
Ile Asn	110					
aatgagctca aggaatcctc ctccctcttt tttttttttt tttttacaaa ttatatatgt						2838
aacacatatt cactgcagaa aaattagaaa acacagataa accaaaaaga aaaaaaatta						2898
tagttcccca aatggggcac agaagaccca gtggacatag aagtgtgata gacttggatt						2958
taaaactgggt accagtatgt gacccctggac aagtcactga attgttttgt tcttccattc						3018
ccttatctat agaattggga tgataaact ttaaaagggt cttgtaagga ttaaaaatgtg						3078
ataatatata aagatttttg cataatgcct gccctgtgct gtgcttagta ccttagttta						3138
gacgctttgc aaccccatgg actgtagccc accaggctcc tctgtccatg tggattctgc						3198
aggaagaat actggagttg gtcaccatgc actcctccag gggatcttcc caactcaggg						3258
atcgaaccca ggtccttagcc tacagtatta attgatgtgt ttattttttac ttttatccca						3318
ctagctagag cacatcatcc tagacatttt gatacatggc ctaccaattt gtgtccagtg						3378
taagaatata catgtgtgtg ctacgtggct cagtcgtgtc tgactctttg caaccccatg						3438
gactgtagcc cgcgaagct cctctgccca tgggattgcc cagccaagaa tactggagca						3498
ggttgccatt tcttctccca ggggatcttt caacacaggg attgaatcct tgtctctctg						3558
gtttctctga ttggcaggtg tattctttac cactgagcca cctgggaaac ccttaagta						3618
tatacatca aatcttttat agtttccatt ctcccttcta ccactccaaa tgggtatac						3678
caaggagaa gtatttttgt agctaggcag tattcctgga gccctctctt gggagtcag						3738
ttaaagggtt ttgtgtacag tgaggaaatgc cagggaattga gggagacttg ctgtcttctt						3798
ttcag gg agc cag gtg tgg gga gga cag ctg gta tat ccc aca gaa cct						3847
Gly Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro	115	120	125			
gat gat acc tgc atc ttc ccc gat ggg gag ccc tgc cct tct ggc cct						3895
Asp Asp Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro	130	135	140			
cta tct cag aaa aga tgc ttt gtt tat gtc tgg aag acc tgg g						3938
Leu Ser Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp	145	150	155			

SEQCRF05081156

gtaagaggttt	cccttctctg	gcctgtcatt	cacacttaaa	ttcacttctt	cttacctgat	3998
cccccttctt	ttgggtctcat	ccttaaaattc	tgtgagtttc	cctaattcttc	acttccccca	4058
tgactctctt	ctcttccaca	gcaccttagtc	aactctatta	tacttctttc	tgggagccct	4118
gtctcaatta	tagtcccatc	ccatggagccc	tctcataagg	actttttttc	tgcccaacat	4178
atgcaagctt	aaactctctg	aaataaacat	ccttgataca	tctcctgacc	ttccttctct	4238
ggttcacatc	ctaaccctgc	cccagtcctcc	tttgaccagt	aaccccccttc	cttactcttc	4298
ttttcaaaaa cctcag ac caa tac tgg caa gtt ctg ggg ggc cca gtg tct						4349
Asp Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser						
160 165						
gga ctg agc atc ggg aca gac aag gca atg ctg ggc aca tat aac atg	4397					
Gly Leu Ser Ile Gly Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met						
170 175 180						
gaa gtg act gtc tac hac cgc cgg ggg tcc cag agc tat gtg ccc ctc	4445					
Glu Val Thr Val Tyr His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu						
185 190 195 200						
gct cac tcc agt tca gcc ttc acc att act g gtaaggactg aggaggggac	4496					
Ala His Ser Ser Ser Ala Phe Thr Ile Thr						
205 210						
aaggccagtt gcagggcagg agaaggtggg gaggctgggc tggacaggaa aggggaaaga	4556					
agaaatgggt tgtaacctta caggggcaga accaggaaga tgtgggcaga gggatgtggg	4616					
gcttgagacc cgtgaagggc caggcagctt gggttgggtg aaaaatatgg ctgtgaaaga	4676					
agaagctgac agaaagaaga acttatggtt ctcactttct ctgactccaa tccca gac	4734					
Asp						
cag gtg ccc ttc tct gtg agt gtg tct cag ctg cag gcc ttg gat gga	4782					
Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala Leu Asp Gly						
215 220 225						
agg aac aag cgc ttc ctg aga aag cag cct ctg acc ttt gcc ctc cag	4830					
Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe Ala Leu Gln						
230 235 240						
ctc cat gat ccc agt ggc tat ttg gct ggg gct gac ctt tcc tac acc	4878					
Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu Ser Tyr Thr						
245 250 255						
tgg gac ttt ggt gac agt aca ggg acc ctg atc tct cgg gca ctc acg	4926					
Trp Asp Phe Gly Asp Ser Thr Ser Gly Thr Leu Ile Ser Arg Ala Leu Thr						
260 265 270 275						
gtc act cac act tac cta gag tct ggc cca gtc act gca cag gtg gtg	4974					
Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala Gln Val Val						
280 285 290						
ctg cag gct gcc att cct ctc acc tcc tgt ggc tcc tct cca gtt cca	5022					
Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser Pro Val Pro						
295 300 305						
ggc act aca gat agg cat gtg aca act gca gag gct cct gga acc aca	5070					
Gly Thr Thr Asp Arg His Val Thr Thr Ala Glu Ala Pro Gly Thr Thr						
310 315 320						
gct ggc caa gtg cct act aca gaa gtc atg ggc acc aca cct ggc cag	5118					
Ala Gly Gln Val Pro Thr Thr Glu Val Met Gly Thr Pro Gly Gln						
325 330 335						

SEQCRF05081156

gtg cca act gca gag gcc cct ggc acc aca gtt ggg tgg gtg cca acc Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp Val Pro Thr 340 345 350 355	5166
aca gag gat gta ggt acc aca cct gag cag gtg gca acc tcc aaa gtc Thr Glu Asp Val Gly Thr Thr Pro Glu Val Val Ala Thr Ser Lys Val 360 365 370	5214
tta agt aca aca cca gtg gag atg cca act gca aaa gct aca ggt agg Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala Thr Gly Arg 375 380 385	5262
aca cct gaa gtg tca act aca gag ccc tct gga acc aca gtt aca cag Thr Pro Glu Val Ser Thr Thr Pro Ser Gly Thr Thr Val Thr Glu 390 395 400	5310
gga aca act cca gag ctg gtg gag acc aca gct gga gag gtg tcc act Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu Val Ser Thr 405 410 415	5358
cct gag cct gcg ggt tca aat act agc tca ttc atg cct aca gaa ggt Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro Thr Glu Gly 420 425 430 435	5406
act gca g gtaagggggc caccatgaat gaggttcatag aggtgggggca tttgtcacag Thr Ala	5463
ctctgaagac ctgaaagaat tgctcaggac ccagatgtta ctcaatcctt agcttagcacg tggagtcctcc tcagaaatctt cactgtgtttt aaaacccctt aagtcctctt taatggcac gaatagatcc agaggttcagg aaaccagggt ctctctcctag gccagggtgtta gacaggttat ttctctcttc tgaagagaagc ttccaggaagc agtgtgtgat catttggttg tgggtctcag tcattgtctga ctctttgtga cctcatggac tatggccccc caggctcttc tgtccataga attctccagg caagaacct ggagtggttg gccatttctt tctccagggg attttccctg cccagggtatt aaaccggaat tggcaggttg attctttacc cgagccacct agaaagtccc atgtgatcat tagataatc ttatacctca tttcttgatt aagtgttaaac acagaaatct ttctgacacc acttcccacc cctggattcc catcccaag taggtttacc tgggaattgtg gtaggaatc taaaaaggga gaagtgtgat agtgacacta tgacttaaca catgtcaaat gtctgaccca ggacctggca cagtgtatggg tgtgataaac atttgggatg tctaaaattc tgactctaac cctgtgactc tggggcagtc atttctcttg ggcctttctt tatcttaaaa aatgagagtt tccagctctt gtctgattct aagccttgat ccagtagctc tgactctacc tggaaaaatt ctgtttgggc ctgttttcatt tgccttttga ctgttcctct	5523 5583 5643 5703 5763 5823 5883 5943 6003 6063 6123 6183 6243 6303
ttaatcctct cctccag gc tcc ctg agt ccc ctg ccg gat gac act gcc Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala 440 445	6352
acc tta gtc ctg gag aag cgc caa gcc ccc ctg gat tgt gtt ctg tat Thr Leu Val Leu Glu Lys Arg Glu Ala Pro Leu Asp Cys Val Leu Tyr 450 455 460	6400
cgc tat ggc tcc ttt tcc ctc acc ctg gac att gtc c gtgagtcttg Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val 465 470 475	6447
cctacattgt ccgtaagctg gtggaggag gcgtgtgctg cttaggggtg ccagtgga gcacaccttg gaaggaatta ctacactgga caaggagaat accagatcc cagggggttc atatgaaggc agaatggag tagggaggca gcccgaggac ctctctggcc atgggccttg	6507 6567 6627
ggggaggata agtagaggag tctcagactt aaaaaaatct tgcaactttg cag ag Gln	6682

SEQCRF05081156

ggt att gag agt gct gag atc cta cag gct gtg tca tcc agt gaa gga Gly Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly 480 485 490	6730
gat gca ttt gag ctg act gtg tct tgc caa ggc gg gtgagtgtcc Asp Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly 495 500 505	6775
cacggttgcc ctgagaactc ctggggtgac tgctgtcctg ttctctgggtg tctagtgtcc	6835
cttcccgatg tccctgacgt aagctgacat ctctcccg g cta ccc aag gaa gcc Leu Pro Lys Glu Ala 510	6890
tgc atg gac atc tca tgc cca ggg tgt cag ctg cct gcc cag cgg ctg Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu 515 520 525	6938
tgt cag cct gtg ccc ccc agc cca gcc tgc cag ctg gtt ttg cac cag Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln 530 535 540	6986
gta ctg aag ggt ggc tca ggg acc tac tgc ctc aat gtg tct ttg gct Val Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala 545 550 555	7034
gat gcc aat agc ctg gcg atg gtc agc acc cag ctt gtc atg cct g Asp Ala Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro 560 565 570	7080
gtaggtagtt ggacaagagg taggatgaag acacggggag atggtagagg ttacctacta	7140
gaggaagcag acactgaatg cagccgtatc tgggattcca cccatag gg caa gaa Gly Gln Glu 575	7195
gca ggc ctc agg cag gct cct ctg ttc gtg ggc atc ttg ctg gtg cta Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu 580 585 590	7243
aca gct ttg ttg ctt gca tct ctg ata tac ag gtgagatccc cgccatcctg Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg 595 600	7295
ctccactcc tttacccttt attaccacca ccactcttcc tcatgggaag aagaaccac caaccctttt gggaaagtgt agagtccaag aaagagccca gacttggaag ttcaacaggt ctaggctgca gtcttgctgtg tgggaccctg ggggaagtcca ttaacccttc tgagccactg aaaagttaga aacataatac ctgtctctgt gggctgtttt cagggctcta gacaatgtga tgaataatat caacagtggg acaaaaagtgg aataaatgat gatccaatg actgtttgta tgaataatat caacagtggg gaagaactca gtgaactgag ttctccacct gccagaaagg caaatcccta ggcctggagg gctgaggtcc tcaaagcagg gaagcctgta ggggtgagagg gaaatgtgta gagcttacca taacataag agaggataaa cctgtttggt gagaagagg gggagccagg atcaagacca agtcaacctg ggttatgttt tagtcttttt tttttagaga agcacaaga ggttgccatt gaccaccact aaccagtatc cctgcttttc tcccaatatc 605 610 615	7355 7415 7475 7535 7595 7655 7715 7775 7835 7895
ag g cga aga ctt atg aag caa ggc tca gca gtc ccc ctt ccc cag ctg Arg Arg Leu Met Lys Gln Gly Ser Ala Val Pro Leu Pro Gln Leu 605 610 615	7943
cca cac ggt aga acc cag tgg cta cgt ctg ccc tgg gtc ttc cgc tct Pro His Gly Arg Thr Gln Trp Leu Arg Leu Pro Trp Val Phe Arg Ser	7991

SEQCRF05081156

620

625

630

tgc ccc att ggt gag agc aaa ccc ctc ctc agt gga cag cag gtc 8036
 Cys Pro Ile Gly Glu Ser Lys Pro Leu Leu Ser Gly Gln Gln Val
 635 640 645

tgagtgtctc tatgtgaagt catgatttac ccaggtggac agcaaggcct gtcttttctc 8096
 tggctctccc tcagagacta ccattgcctg aaataaagac tcagaacttg 8146

<210> 4
 <211> 649
 <212> PRT
 <213> Bos taurus

<400> 4
 Met Asp Leu Val Leu Arg Lys Tyr Leu Leu His Val Ala Leu Met Gly
 1 5 10
 Val Leu Leu Ala Val Arg Thr Thr Glu Gly Pro Arg Asp Arg Asp Trp
 20 25 30
 Leu Gly Val Ser Arg Gln Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu
 35 40 45
 Tyr Pro Glu Trp Thr Glu Ser Gln Gly Pro Asp Cys Trp Arg Gly Gly
 50 55 60
 His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
 65 70 75 80
 Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser Gln Lys Val
 85 90 95
 Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly
 100 105 110
 Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro Asp Asp
 115 120 125
 Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro Leu Ser
 130 135 140
 Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp Asp Gln Tyr Trp
 145 150 155 160
 Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Asp Lys
 165 170 175
 Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr His Arg Arg
 180 185 190
 Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ala Phe Thr
 195 200 205
 Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala
 210 215 220
 Leu Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe
 225 230 235 240
 Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu
 245 250 255

SEQCRF05081156

Ser Tyr Thr Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg
 260 265 270
 Ala Leu Thr Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala
 275 280 285
 Gln Val Val Leu Gln Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser
 290 295 300
 Pro Val Pro Gly Thr Thr Asp Arg His Val Thr Thr Ala Glu Ala Pro
 305 310 315 320
 Gly Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Met Gly Thr Thr
 325 330 335
 Pro Gly Gln Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp
 340 345 350
 Val Pro Thr Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr
 355 360 365
 Ser Lys Val Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala
 370 375 380
 Thr Gly Arg Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr
 385 390 395 400
 Val Thr Gln Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu
 405 410 415
 Val Ser Thr Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro
 420 425 430
 Thr Glu Gly Thr Ala Gly Ser Leu Ser Pro Leu Pro Asp Thr Ala
 435 440 445
 Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr
 450 455 460
 Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val Gln Gly Ile Glu
 465 470 475 480
 Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly Asp Ala Phe
 485 490 495
 Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met
 500 505 510
 Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu Cys Gln
 515 520 525
 Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Val Leu
 530 535 540
 Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala
 545 550 555 560
 Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly Gln Glu
 565 570 575
 Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu
 580 585 590

SEQCRF05081156

Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys
 595 600 605
 Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg Thr Gln
 610 615 620
 Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser
 625 630 635 640
 Lys Pro Leu Leu Ser Gly Gln Gln Val
 645

<210> 5
 <211> 8143
 <212> DNA
 <213> Bos taurus

<220>
 <221> CDS
 <222> (30)..(101)
 <223> First CDS region

<220>
 <221> CDS
 <222> (2323)..(2432)
 <223> Second CDS region

<220>
 <221> CDS
 <222> (2579)..(2724)
 <223> Third CDS region

<220>
 <221> CDS
 <222> (3801)..(3934)
 <223> Fourth CDS region

<220>
 <221> CDS
 <222> (4312)..(4472)
 <223> Fifth CDS region

<220>
 <221> CDS
 <222> (4730)..(5409)
 <223> Sixth CDS region

<220>
 <221> CDS
 <222> (6318)..(6433)
 <223> Seventh CDS region

<220>
 <221> CDS
 <222> (6678)..(6762)
 <223> Eighth CDS region

<220>
 <221> CDS
 <222> (6873)..(7076)
 <223> Ninth CDS region

SEQCRF05081156

<220>
 <221> CDS
 <222> (7185)..(7272)
 <223> Tenth CDS region

<220>
 <221> CDS
 <222> (7896)..(8033)
 <223> Eleventh CDS region

<400> 5
 ggtctttggt tgctggaagg aagaacagg atg gat ctg gtg ctg aga aaa tac 53
 Met Asp Leu Val Leu Arg Lys Tyr
 1 5

ctt ctc cat gtg gct ctg atg ggt gtt ctg gct gta ggg acc aca gaa g 102
 Leu Leu His Val Ala Leu Met Gly Val Leu Ala Val Gly Thr Thr Glu
 10 15 20

gtgagtgtgg gatgttggac atgaacaagt gtgaatttgg ggttgacac ctgctctggt 162
 ttttctctcc ctataatgga agatatcagt agtgcttcag gtgtctccca cccatttggat 222
 ttagtgagga catggggcaac tgagctccct ccccatatga agatttgggt gcatgtgtgt 282
 tcaggcactt gggactgaac ctgaaaacaa ccccatctac ctggatgggt gagagaacag 342
 tatgtctccg tggccctaatt ttgagatgc tctgaatagt gagctggaac atgggtgcca 402
 aggtagttaa atgagtggaa actcatttag gctttgtctc aggcacttgg gatagggtat 462
 ttaggagata gagaaagata ggagatagga gaaaggagaa agaggatgtg gtattggata 522
 gaaggtaaat gaggcacctt atcccccttt tgggatgggc atgggtgaac acagcccagg 582
 cttttgttct ggggctggaa gagacaggca gaagggtctc agctgagcat cacatgaaag 642
 ggctctgggg gatttggggcc tctgtacagg agcaaggcgg gtgggggtgg gatggtgaga 702
 ggggtctggaa tgtcccgctg tctcttggag agggaggaatt gggagtggag aaagaatggg 762
 gcatcttatg attctcttgt tcttctgggt aggtattcag tgggataatt ctatgacctc 822
 ccccaagaga atcaaccagg ttctctgttac atgttagaga tggagtggag atagtctgtg 882
 atgtgcagaa atatatcaat tgtaccctag tgcccccttt ccttagatctc ctggtctcac 942
 agactctctg gaactctctc ttgatctgac ttccctcatt catgggtgtca ttccaagtct 1002
 tattctttta ctatgtctgt tattgtattc tggaaatadc ctgttcatat gtgtccacc 1062
 aaggctctta atatgtttgt cttacttttt ggaaccagat ttttaaaatc ataagaagac 1122
 attttatat agttcatgaa attttgcatt gactgagttt gataattttg tttagtgtga 1182
 attaacattt tgtttattta agaaaaaaaa atattttttt acagaaacct actgaatttg 1242
 tagggtttta aaataacatg atgtctggga ttgtcttttg aatgcttcag ccaaaaaaca 1302
 aacgaacaac aaaaaataag gatagataaa gcaaatgtga caaaatgctg atagtgtgtg 1362
 gactcttggg agacacatgc agacccatca catcactttt ttccagactt ctttcttgggt 1422
 cagttataat catttttgtt gtccccctac ccaattttcta ctgtccctca gtccatctct 1482
 ctactgtctt gccaaaagta atgtccata tatcagtaca acacaaaatc gatcatattc aaaaagcttt 1542
 tgaagggtaa gttttatggt atatgccata tatcagtaca acacaaaata tcgtctgagg 1602
 tgccgttgcg ccaaaagata atgtccaaact cctttgctgt gcaactcagg ccccatctct 1662
 atcttcttgg cctcatctct catgatgtac atcagccaca ttgtagtgtt ctgtctatgg 1722
 ctcttctgct agaattgctt atgtccccga caactattta ctgtcttctt cagtgcacca 1782
 gagtgcattt tacctgttta aaatctatca ttttgttata cattgtgcat gtctattatg 1842
 gctcatatta agcaatgctt tggattatag taatttatgt taatttatgt tctatatact 1902
 ttaacctgaa ccccttcaga accatttctt tttcatttct taagtcttct gcaactagcc 1962
 cagtcctggy tagctctggy gatttcagta gattaaaatg cactttaagg aacttccctt 2022
 gtgtgccatc aagtgtgcta ggctctgtgc tcccaatgca ggggaccagg gttcaatctc 2082
 aggtcaggga actagatccc acaggtcaca actaagagtt tgcaagccac aactacttga 2142
 cctcacatgc cacaactaat cgaagatccc tctgtctgca actaagctct agtgcagtta 2202
 aatatatttt tttaatgcac ttggaatgtg agaattgaat atgtgtcaca gacactgttg 2262
 tcccctgaga agggagttag taatgatatt agggccctca tagtatattc tcctttttag 2322

ga ccc aga gac agg gac tgg ctt ggt gtc tca agg cag ctc aga att 2369
 Gly Pro Arg Asp Arg Asp Trp Leu Gly Val Ser Ile
 25 30 35 40

aaa gca tgg aac aga cag ctg tat cca gag tgg aca gaa agc cag ggg 2417

SEQCRF05081156

Lys	Ala	Trp	Asn	Arg 45	Gln	Leu	Tyr	Pro	Glu 50	Trp	Thr	Glu	Ser	Gln 55	Gly	
cct	gac	tgc	tgg	aga	g	gtagga	actt	ggc	aattt	tcc	aggg	aggata	tgg	tgg	ggaat	2473
Pro	Asp	Cys	Trp	Arg												
			60													
gggt	ggggag	ggga	acgggg	ttga	atgtac	ttagga	agat	agga	agagaa	aagg	cgata					2533
gggagg	gagaa	gccaa	ggagc	taatta	atgc	agctg	ccctt	ttcag	gt	ggc	cac	ata				2589
									Gly	Gly	His	Ile				
												65				
tcc	ctg	aag	gtc	agc	aat	gat	ggg	cct	aca	ctg	att	ggg	gca	aat	gct	2637
Ser	Leu	Lys	Val	Ser	Asn	Asp	Gly	Pro	Thr	Leu	Ile	Gly	Ala	Asn	Ala	
				70												
tcc	ttc	tct	att	gcc	ttg	cac	ttt	cct	aaa	agc	caa	aag	gtg	ctg	cca	2685
Ser	Phe	Ser	Ile	Ala	Leu	His	Phe	Pro	Lys	Ser	Gln	Lys	Val	Leu	Pro	
			85					90					95			
gat	ggg	cag	gtc	atc	tgg	gcc	aac	aac	acc	atc	atc	aat	g	gtg	agtac	2735
Asp	Gly	Gln	Val	Ile	Trp	Ala	Asn	Asn	Thr	Ile	Ile	Asn				
			100				105					110				
ctccgc	ctctc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	2795
ctccct	ctctt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	2855
aaattag	aaaaa	acacag	atata	aaac	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	aaaaa	2915
agaagac	acaca	gtggac	atagat	aaagt	gggata	aaagt	gggata	aaagt	gggata	aaagt	gggata	aaagt	gggata	aaagt	gggata	2975
gaccct	gggac	aaagt	ctac	gtg	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3035
tgataac	actt	ttaaa	agggt	ctt	gtta	aggat	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3095
cataat	gcct	gccct	gtgct	gtg	ctt	tagta	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3155
actgtag	cccc	accagg	gtct	ctg	ttc	ccatg	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3215
gtcacat	gc	actcc	ctcag	gtg	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3275
tacagt	atta	attgat	gtct	gtg	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3335
tagacatt	tt	gatac	atagc	gtg	ctt	accaa	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3395
ctcagt	ggct	cagt	ctgt	gtc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3455
ctctgt	ccca	tggg	attt	gcc	atg	cca	agaa	tact	ggag	ca	ggtt	gccatt	ttct	ctct	cca	3515
ggggat	cttt	caac	acaggg	gt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	3575
tattct	ttac	cact	gagcca	ct	ggg	aaac	ccct	taag	ta	ta	ca	acata	aat	cttt	ttt	3635
agttt	ccatt	ct	ccctt	cta	ctt	ccca	aa	gggt	ttat	ac	aggaga	aat	gtatt	ttt	gtt	3695
agctag	gcag	tatt	ctctga	gt	ccct	ctct	ct	ggg	agtc	atg	ttaa	agggtt	tgg	gtac	ag	3755
tgagga	aatgc	caggg	attga	ggg	agact	gtg	cttctt	ttc	ag	gg	agc	cag	gtg			3811
											Gly	Ser	Gln	Val		
tgg	gga	gga	ctg	gta	tat	ccc	pro	caa	gaa	cct	gat	gat	acc	tgc	atc	3859
Trp	Gly	Gly	Gln	Leu	Val	Tyr	Pro	Gln	Glu	Pro	Asp	Asp	Thr	Cys	Ile	
115										125					130	
ttc	ccc	gat	ggg	gag	ccc	tgc	cct	tct	ggc	cct	cta	tct	cag	aaa	aga	3907
Phe	Pro	Asp	Gly	Glu	Pro	Cys	Pro	Ser	Gly	Pro	Leu	Ser	Gln	Lys	Arg	
				135					140					145		
tgc	ttt	ggt	tat	gtc	tgg	aag	acc	tgg	g	gta	agag	ttt	ccctt	ctctg		3955
Cys	Phe	Val	Tyr	Val	Trp	Lys	Thr	Trp								
			150					155								
gcctgt	catt	cacact	taaa	ttt	taact	ttct	cct	act	ctt	ccca	gtt	ccctt	ttct	ttt	gtct	4015
cccttaa	ttt	tgtg	agttt	ctt	taact	ttct	act	ctt	ccca	gtt	gtact	ctctt	ctt	ctt	ccaca	4075
gcac	ctag	aat	cttata	tact	tttt	ctt	ggg	agcc	ct	gtcca	att	ta	gtc	ccat	ct	4135
ccatgg	agcc	ttcata	aaqg	act	tttt	ctt	ggc	caact	ct	atgca	agtt	aa	act	ctct	ctg	4195

SEQCRF05081156

aaataacccat ccttgataca tctcctgacc ttccttctct ggttccatct ctaaccctgc	4255
cccagctctcc ttggaccagt aaccccccttc cctactcttc ttccaaaaa cctcag ac	4313
	Asp
caa tac tgg caa gtt ctg ggg ggc cca gtg tct gga ctg agc atc ggg	4361
Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly	
	160
aca gac aag gca atg ctg ggc aca tat aac atg gaa gtg act gtc tac	4409
Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr	
	175
cac cgc cgg ggg tcc cag agc tat gtg ccc ctc gct cac tcc agt tca	4457
His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser	
	190
gcc ttc acc att act g gtaaggactg aggaggggac aaggccagtt gcagggcagg	4513
Ala Phe Thr Ile Thr	
	205
agaaggtggg gaggctgggc tggacaggaa aggggaaaga ggaaatggtg tgtaacctta	4573
caggggcaga accaggaaga tgtgggcaga gggatgtggg gcttggagcc cgtgaagggc	4633
caggcagctt ggggtggtg aaaaatatgg ctgtgaaaga agaagctgac agaaagaaga	4693
acttatggtt ctcactttct ctgactccaa tcccag ac	4746
	Asp
	210
gtg agt gtg tct cag ctg cag gcc ttg gat gga agg aac aag cgc ttc	4794
Val Ser Val Ser Gln Leu Gln Ala Leu Asp Gly Arg Asn Lys Arg Phe	
	220
ctg aga aag cag cct ctg acc ttt ggc ctc cag ctc cat gat ccc agt	4842
Leu Arg Lys Gln Pro Leu Thr Phe Ala Leu Gln Leu His Asp Pro Ser	
	235
ggc tat ttg gct ggg gct gac ctt tcc tac acc tgg gac ttt ggt gac	4890
Gly Tyr Leu Ala Gly Ala Asp Leu Ser Tyr Thr Trp Asp Phe Gly Asp	
	250
agt aca ggg acc ctg atc tct cgg gca ctc acg gtc act cac act tac	4938
Ser Thr Gly Thr Leu Ile Ser Arg Ala Leu Thr Val Thr His Thr Tyr	
	265
cta gag tct ggc cca gtc act gca cag gtg gtg ctg cag gct gcc att	4986
Leu Glu Ser Gly Pro Val Thr Ala Gln Val Val Leu Gln Ala Ala Ile	
	280
cct ctc acc tcc tgt ggc tcc tct cca gtt cca ggc act aca gat agg	5034
Pro Leu Thr Ser Cys Gly Ser Ser Pro Val Pro Gly Thr Thr Asp Arg	
	300
cat gtg aca act gca gag gct cct gga acc aca gct ggc caa gtg cct	5082
His Val Thr Thr Ala Glu Ala Pro Gly Thr Thr Ala Gly Gln Val Pro	
	315
act aca gaa gtc atg ggc acc aca cct ggc cag gtg cca act gca gag	5130
Thr Thr Glu Val Met Gly Thr Thr Pro Gly Gln Val Thr Thr Ala Glu	
	330
gcc cct ggc acc aca gtt ggg tgg gtg cca acc aca gag gat gta ggt	5178

SEQCRF05081156

Ala	Pro	Gly	Thr	Thr	Val	Gly	Trp	Val	Pro	Thr	Thr	Glu	Asp	Val	Gly	
345						350						355				
acc	aca	cct	gag	cag	gtg	gca	acc	tcc	aaa	gtc	tta	agt	aca	aca	cca	5226
Thr	Thr	Pro	Glu	Gln	Val	Ala	Thr	Ser	Lys	Val	Leu	Ser	Thr	Thr	Pro	
360					365					370					375	
gtg	gag	atg	cca	act	gca	aaa	gct	aca	ggt	agg	aca	cct	gaa	gtg	tca	5274
Val	Glu	Met	Pro	Thr	Ala	Lys	Ala	Thr	Gly	Arg	Thr	Pro	Glu	Val	Ser	
				380					385					390		
act	aca	gag	ccc	tct	gga	acc	aca	ggt	aca	cag	gga	aca	act	cca	gag	5322
Thr	Thr	Glu	Pro	Ser	Gly	Thr	Thr	Val	Thr	Gln	Gly	Thr	Pro	Pro	Glu	
			395					400					405			
ctg	gtg	gag	acc	aca	gct	gga	gag	gtg	tcc	act	cct	gag	cct	gcg	ggt	5370
Leu	Val	Glu	Thr	Thr	Ala	Gly	Glu	Val	Ser	Thr	Pro	Glu	Pro	Ala	Gly	
			410				415					420				
tca	aat	act	agc	tca	ttc	atg	cct	aca	gaa	ggt	act	gca	g	gtaagggggc		5420
Ser	Asn	Thr	Ser	Ser	Phe	Met	Pro	Thr	Glu	Gly		Ala				
	425					430					435					
caccatgaat	gagttcatag	agggtgggca	tttgtcacag	ctctgaagac	ctgaagaagt	5480										
tgctcaggac	ccagatgtta	ctcaatcctt	agcttagcac	tggagtcctc	tcagaatctt	5540										
cactggtttt	aaaaccccc	aagtccctct	taatggcaca	gaatagatcc	agagttcagg	5600										
aaaccagggt	cttctcctag	gccaggggta	gagagcttat	ctctcttccc	tgaagagaag	5660										
ttcaggaagc	agtgtgtgat	catttgggtg	tgtgtctcag	ctatgtctga	ctcttcttga	5720										
ctctatggac	tatggccac	caggctcttc	tgctcataga	attctccagg	caagaacact	5780										
ggagtgggtg	gccatttctc	ttctcagggg	attttccctg	cccagggaat	aaacccgaat	5840										
tggcagggtg	attctttacc	cgagccactt	agaaagtccc	atgtgatcat	tagataaatc	5900										
ttataccta	ttttctgatt	aagtgttaac	acagaaatct	ttctgacacc	acttcccacc	5960										
cctggattcc	catcccaag	taggtttacc	tggaaattgt	gtaggaatac	taaaaaagga	6020										
gaagtgtgat	agtgcacta	tgacttaaca	catgtcaaat	gtctgaccca	ggacctggca	6080										
cagtgtaggg	tgtgataaac	atttgggatg	tctaaaaatc	tgacttctaac	cctgtgactc	6140										
tggggcagtc	atttctcttg	ggcctttctt	tatcttaaaa	aatgagagtt	tccagctctt	6200										
gtctgattct	aagccctggat	ccagttagctc	tgactctacc	tggaaaaaatg	cttgttgggc	6260										
ctgttttcag	gttagtcatt	tgctttttga	ctttgcctct	ttaatcctct	cctccag	6317										
gc	tcc	ctg	agt	ccc	ctg	ccg	gat	gac	act	gcc	acc	tta	gtc	ctg	gag	6364
Gly	Ser	Leu	Pro	Pro	Leu	Pro	Asp	Asp	Thr	Ala	Thr	Leu	Val	Leu	Glu	
			440					445					450			
aag	cgc	caa	gcc	ccc	ctg	gat	tgt	gtt	ctg	tat	cgc	tat	ggc	tcc	ttt	6412
Lys	Arg	Gln	Ala	Pro	Leu	Asp	Cys	Val	Leu	Tyr	Arg	Tyr	Gly	Ser	Phe	
			455				460					465				
tcc	ctc	acc	ctg	gac	att	gtc	c	gtgagtcctg	cctacattgt	ccgtaagctg						6464
Ser	Leu	Thr	Leu	Asp	Ile	Val										
			470			475										
gtggaggggag	gcgtgtgctg	cttaggggtg	cccagtgaa	gcacaccttg	gaaggaatta	6524										
ctcacctgga	caaggagaat	accagatccc	cagggggttc	atatgaaggc	agaatgggat	6584										
tagggaggca	gcccaggagc	cttcttgccc	atgggccttg	ggggaggata	agtagaggag	6644										
tctcagactt	aaaaaaaaatct	tgcaactttg	cag	ag	ggt	att	gag	agt	gct	gag						6697
				Gln	Gly	Ile	Glu	Ser	Ala	Glu						
									480							
atc	cta	cag	gct	gtg	tca	tcc	agt	gaa	gga	gat	gca	ttt	gag	ctg	act	6745
Ile	Leu	Gln	Ala	Val	Ser	Ser	Ser	Glu	Gly	Asp	Ala	Phe	Glu	Leu	Thr	
			485				490					495				

SEQCRF05081156

gtg tct tgc caa ggc gg	gtgagtgtcc	cacggttgcc	ctgagaactc	6792
Val Ser Cys Gln Gly Gly				
500				
ctgggggtgac tgctgtcctg	ttctctgggtg	tctagtgtcc	cttcccagat tccctgacgt	6852
aagctgacat ctctccag g	cta ccc aag gaa gcc tgc atg gac atc tca			6902
	Leu Pro Lys Glu Ala Cys Met Asp Ile Ser			
505	510			
tcg cca ggg tgt	cag ctg cct gcc	cag cgg ctg tgt	cag cct gtg ccc	6950
Ser Pro Gly Cys Gln Leu	Pro Ala Gln Arg	Leu Cys Gln Pro Val	Pro	
515	520	525	530	
ccc agc cca gcc	tgc cag ctg gtt	ttg cac cag gta	ctg aag ggt ggc	6998
Pro Ser Pro Ala Cys Gln	Leu Val Ser His	Gln Val Leu Lys	Gly Gly	
535	540	545		
tca ggg acc tac	tgc ctc aat gtg	tct ttg gct gat	gcc aat agc ctg	7046
Ser Gly Thr Tyr	Cys Leu Asn Val Ser	Leu Ala Asp Ala Asn	Ser Leu	
550	555	560		
gcg atg gtc	agc acc cag ctt	gtc atg cct g	gtaggtagtt ggacaagagg	7097
Ala Met Val Ser Thr Gln	Leu Val Met Pro			
565	570			
taggatgaag acacggggag	atggtagagg	ttacctacta	gaggaagcag acactgaatg	7157
cagccgtatc tgggattcca	cccatag gg	caa gaa gca ggc ctc	agg cag gct	7210
	Gly Gln Glu Ala Gly Leu Arg Gln Ala			
	575	580		
cct ctg ttc gtg	ggc atc ttg ctg	gtg cta aca gct	ttg ttg ctt gca	7258
Pro Leu Phe Val Gly Ile	Leu Leu Val Leu Thr Ala Leu Leu Ala			
585	590	595		
tct ctg ata tac ag	gtgagatccc	cgccatcctg	ctcccactcc tttaccctt	7312
Ser Leu Ile Tyr Arg				
600				
attaccacca ccactcttcc	tcattgggaag	aagaaaccac	caaccctttt gggaaagtgt	7372
agagttccaa aagagcccca	gacttgggaag	ttcaacaggt	ctaggctgca gtcctgtctgg	7432
tgggaccctg ggggaagtcca	ttaaccttcc	tgagccactg	aaaagttagga aacataatcc	7492
ctgtcctgtg gggctgtttt	cagggcctcta	gacaatgtga	gtaaaaacacc tgggtctgaa	7552
acaaaagtgg aataaatgat	gatctcaatg	actgtttgta	tgaataatat caacagtgga	7612
gaagaactca gtgaactgag	ttctccacct	gccagaaaagg	caaatcccta ggcctggagg	7672
gctgaggtcc tcaagcagg	gaagcctgta	gggtgagagg	gaaatgggtca gagcttacca	7732
taaacataag agaggataaa	ccctgttggg	gagaagagga	gggagccagg atcaagacca	7792
agtcaacctg ggttatggtt	tagtcttttt	tttttagaga	agcacaaga ggttgccatt	7852
gaccaccat aaccagtatc	cctgcttttc	tcccaatatc		7892
ag g cga aga ctt atg	aag caa ggc	tca gca gtc	ccc ctt ccc cag	7937
Arg Arg Leu Met Lys Gln Gly	Ser Ala Val Pro Leu Pro Gln			
605	610	615		
ctg cca cac ggt	aga acc cag tgg	cta cgt ctg ccc	tgg gtc ttc cgc	7985
Leu Pro His Gly Arg Thr Gln Trp	Leu Arg Leu Pro Trp Val Phe Arg			
620	625	630		
tct tgc ccc att	ggt gag agc aaa	ccc ctc ctc agt	gga cag cag gtc	8033
Ser Cys Pro Ile Gly Glu Ser Lys	Pro Leu Leu Ser Gly Gln Gln Val			
635	640	645		

SEQCRF05081156

tgagtgtctt tatgtgaagt catgattttac ccagggtggac agcaaggcct gtccttttctc 8093

tggtgtctccc tcagagacta ccattgcctg aaataaagac tcagaacttg 8143

<210> 6
<211> 648
<212> PRT
<213> Bos taurus

<400> 6
Met Asp Leu Val Leu Arg Lys Tyr Leu Leu His Val Ala Leu Met Gly
1 5 10 15
Val Leu Ala Val Gly Thr Thr Glu Gly Pro Arg Asp Arg Asp Trp Leu
20 25 30
Gly Val Ser Arg Gln Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu Tyr
35 40 45
Pro Glu Trp Thr Glu Ser Gln Gly Pro Asp Cys Trp Arg Gly Gly His
50 55 60
Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala Asn
65 70 75 80
Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser Gln Lys Val Leu
85 90 95
Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly Ser
100 105 110
Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro Asp Asp Thr
115 120 125
Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro Leu Ser Gln
130 135 140
Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp Asp Gln Tyr Trp Gln
145 150 155 160
Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Asp Lys Ala
165 170 175
Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr His Arg Arg Gly
180 185 190
Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr Ile
195 200 205
Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala Leu
210 215 220
Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe Ala
225 230 235 240
Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu Ser
245 250 255
Tyr Thr Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg Ala
260 265 270
Leu Thr Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala Gln

SEQCRF05081156

275 280 285

Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser Pro
290 295 300

Val Pro Gly Thr Thr Asp Arg His Val Thr Thr Ala Glu Ala Pro Gly
305 310 315 320

Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Met Gly Thr Thr Pro
325 330 335

Gly Gln Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp Val
340 345 350

Pro Thr Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr Ser
355 360 365

Lys Val Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala Thr
370 375 380

Gly Arg Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr Val
385 390 395 400

Thr Gln Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu Val
405 410 415

Ser Thr Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro Thr
420 425 430

Glu Gly Thr Ala Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala Thr
435 440 445

Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr Arg
450 455 460

Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val Gln Gly Ile Glu Ser
465 470 475 480

Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly Asp Ala Phe Glu
485 490 495

Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Asp
500 505 510

Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu Cys Gln Pro
515 520 525

Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Val Leu Lys
530 535 540

Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala Asn
545 550 555 560

Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly Gln Glu Ala
565 570 575

Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu Thr
580 585 590

Ala Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln
595 600 605

Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg Thr Gln Trp

SEQCRF05081156

610

615

620

Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser Lys
625 630 635 640

Pro Leu Leu Ser Gly Gln Gln Val
645

<210> 7
<211> 294
<212> DNA
<213> Artificial sequence

<220>
<223> Probe

<400> 7
gttgctggaa ggaagaacag gatggatctg gtgctgagaa aataccttct ccatgtggct 60
ctgatgggtg ttcttctggc tgtaggagacc acagaagggt agtgtgggat gttggacatg 120
aacaagtgtg aatttggggg tgcacacctg ctctgggttt tctctccccta aaatggaaga 180
tatcagtagt gcttcagggt tctcccaccc atttgattta gtgaggacat gggcaactga 240
gtcctctccc cacatgaaga ttgggtgca tgtgtgttca ggcacttggg actg 294

<210> 8
<211> 294
<212> DNA
<213> Artificial sequence

<220>
<223> Probe

<400> 8
gttgctggaa ggaagaacag gatggatctg gtgctgagaa aataccttct ccatgtggct 60
ctgatgggtg ttcttctggc tgtaaaggacc acagaagggt agtgtgggat gttggacatg 120
aacaagtgtg aatttggggg tgcacacctg ctctgggttt tctctccccta aaatggaaga 180
tatcagtagt gcttcagggt tctcccaccc atttgattta gtgaggacat gggcaactga 240
gtcctctccc cacatgaaga ttgggtgca tgtgtgttca ggcacttggg actg 294

<210> 9
<211> 291
<212> DNA
<213> Artificial sequence

<220>
<223> Probe

<400> 9
gttgctggaa ggaagaacag gatggatctg gtgctgagaa aataccttct ccatgtggct 60
ctgatgggtg ttcttctggc agggaccaca gaaggtagt gtgggatgtt ggacatgaac 120
aagtgtgaat ttgggtttgc acacctgctc tgggttttct ctccctaaaa tggaaagatg 180
cagtagtctc tcagggtgct cccaccattt tgatttagtg aggcacatgg caactgagct 240
ccctcccccac atgaagattt ggtgtcatgt gtgttcaggc acttgggact g 291

<210> 10
<211> 30
<212> DNA
<213> Artificial sequence

<220>

<223> Primer

<400> 10

gttgctggaa ggaagaacag gatggatctg

30

<210> 11

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 11

cagtcccaag tgcctgaaca cacatgcacc

30

<210> 12

<211> 2086

<212> DNA

<213> Artificial sequence

<220>

<223> synthetic nucleotide

<400> 12

ggtctttggt	tgctggaagg	aagaacagga	tggatctggt	gctgagaaaa	taccttctcc	60
atgtggctct	gatgggtgtt	cttctggctg	taaggaccac	agaaggacc	agagacaggg	120
actggtctgg	tgctcaagg	cagctcagaa	ttaagcatg	gaacagacag	ctgatatccag	180
agtggacaga	agccacaggg	ctgactgct	ggagaggtgg	ccacatatcc	ctgaaggtca	240
gcaatgatgg	gcctacactg	attggggcaa	atgtctctt	ctctattgcc	ttgcactttc	300
ctaaaagcca	aaaggtgctg	ccagatgggc	aggatcatctg	ggccaaacaac	accatcatca	360
atggggagcca	gggtgtggga	ggacagctgg	tatatcccca	agaacctgat	gataacctga	420
tcttccccga	tggggagccc	tgccttctg	gccctctatc	tcagaaaaga	tgtcttgttt	480
atgtctggaa	gacctgggac	caatactggc	aagtctctggg	gggcccagtg	tctggactga	540
gcatcggggc	agacaaggca	atgctgggca	catataacat	ggaagtgaact	gtctaccacc	600
gccggggggc	ccagagctat	gtgccccctg	ctcactccag	ttcagccttc	accattactg	660
accaggtgcc	cttctctgtg	agtgtgtctc	agctgcaggg	cttgatgga	aggaacaagc	720
gcttctgtag	aaagcagcct	ctgacctttg	ccctccagct	ccatgatccc	agtggctatt	780
tggctggggc	tgacctttcc	tacacctggg	actttgttga	cagtacaggg	accctgatct	840
ctcgggcatg	cacggtcact	cagactttac	tagagtctgg	cccatgtact	gcacaggtgg	900
tgctgcaggc	tgccattctc	ctcactctct	gtggctctct	tccagttcca	ggcactacag	960
ataggcatgt	gacaactgca	gaggctcctg	gaaccacagc	tggcccaagt	cttactacag	1020
aagtctggc	caccacacct	ggccaggtgc	caactgcaga	ggccccctgg	accacagttg	1080
gggtgggtgcc	aaccacagag	gatgtaggta	ccacacctga	gcaggtggca	acctccaaag	1140
tcttaagtac	aaccacagtg	gagatgccaa	ctgcaaaaag	tacaggtgag	acacctgaag	1200
tgtaacatc	agagccctct	ggaaaccacag	ttacacaggg	aacaactcca	gagctgtgtg	1260
agaccacagc	tggagaggtg	tcactctctg	agcctgcggg	ttcaataact	agctcattca	1320
tgctacatga	aggtacttga	gtcccctgcc	ggatgacact	gctcacttag	gccaccttag	1380
tccttgagaa	gcgccaagcc	cccttggaat	gtgttctgta	tcgtatggc	tccttttccc	1440
tcacctgtga	cattgtccag	gttattgaga	gtgtgagat	ctacagagct	gtgtcatcca	1500
gtgaaggaga	tgcatttgag	ctgactgtgt	cttgccaagg	cgggtacc	aagggaagcct	1560
gcattgacat	cgcactgcga	gggtgtcagc	tgccctgccca	gcggctgtgt	cagcctgtgc	1620
ccccccagccc	agcctgccag	ctggttttgc	accaggtact	gaagggtggc	tcagggaacct	1680
actgctcaca	tgtgtctttg	gctgatgcca	atagcctggc	gatgtgcagc	accagacttg	1740
tcatgtccag	gcaagaagca	ggcctcaggg	aggctcctct	gttctgtggc	atcttgtctg	1800
tgcttaacag	tttgttgcct	gcactctcta	tatacaggcg	aagacttatg	aagcaaggct	1860
cagcagctccc	ctttcccacg	ctgccacacg	gtagaaccaca	gtggctacgt	ctgcccctgg	1920
cttctcgtct	ttgtcccatt	ggttgagagca	aacctctctc	cagtggagcc	caggtcttag	1980
tgctcttatg	tgaagtcagt	atttaccacg	gtggacagca	aggcctgtct	tttctctggt	2040
cttccctcag	agactaccat	tgcctgaaat	aaagactcag	aacttg		2086

SEQCRF05081156

<210> 13
 <211> 649
 <212> PRT
 <213> bovine SILVER

<400> 13
 Met Asp Leu Val Leu Arg Lys Tyr Leu Leu His Val Ala Leu Met Gly
 1 5 10
 Val Leu Leu Ala Val Arg Thr Thr Glu Gly Pro Arg Asp Arg Asp Trp
 20 25 30
 Leu Gly Val Ser Arg Gln Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu
 35 40 45
 Tyr Pro Glu Trp Thr Glu Ser Gln Gly Pro Asp Cys Trp Arg Gly Gly
 50 55 60
 His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
 65 70 75 80
 Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser Gln Lys Val
 85 90 95
 Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly
 100 105 110
 Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro Asp Asp
 115 120 125
 Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro Leu Ser
 130 135 140
 Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp Asp Gln Tyr Trp
 145 150 155 160
 Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Asp Lys
 165 170 175
 Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr His Arg Arg
 180 185 190
 Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr
 195 200 205
 Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala
 210 215 220

SEQCRF05081156

Leu Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe
 225 230 235 240
 Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu
 245 250 255
 Ser Tyr Thr Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg
 260 265 270
 Ala Leu Thr Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala
 275 280 285
 Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser
 290 295 300
 Pro Val Pro Gly Thr Thr Asp Arg His Val Thr Thr Ala Glu Ala Pro
 305 310 315 320
 Gly Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Met Gly Thr Thr
 325 330 335
 Pro Gly Gln Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp
 340 345 350
 Val Pro Thr Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr
 355 360 365
 Ser Lys Val Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala
 370 375 380
 Thr Gly Arg Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr
 385 390 395 400
 Val Thr Gln Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu
 405 410 415
 Val Ser Thr Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro
 420 425 430
 Thr Glu Gly Thr Ala Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala
 435 440 445
 Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr
 450 455 460
 Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val Gln Gly Ile Glu
 465 470 475 480

SEQCRF05081156

Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly Asp Ala Phe
485 490 495

Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met
500 505 510

Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu Cys Gln
515 520 525

Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Val Leu
530 535 540

Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala
545 550 555 560

Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly Gln Glu
565 570 575

Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu
580 585 590

Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys
595 600 605

Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg Thr Gln
610 615 620

Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser
625 630 635 640

Lys Pro Leu Leu Ser Gly Gln Gln Val
645

<210> 14
<211> 8138
<212> DNA
<213> artificial sequence

<220>
<223> synthetic nucleotide

<400> 14
gttgctggaa ggaagaacag gatggatctg gtgctgagaa aataccttct ccatgtggct 60
ctgatgggtg ttcttctggc tgtaaggacc acagaaggtg agtgtgggat gttggacatg 120
aacaagtgtg aatttgggtg tgcacacctg ctctgggttt tctctcccta aaatggaaga 180
tatcagtagt gcttcagggtg tctccacccc atttgattta gtgaggacat gggcaactga 240
gtccctcccc cacatgaaga tttgggtgca tgtgtgttca ggcacttggg actgaacctg 300
aaaacaaccc catctacctg gatgggtgag agaacagtat gtctccgtgg ccctaatttt 360
gagatgctct gaatatgtag ctggaacatg ggtgccaaagg tagtaaaatg agtggaaact 420
catttaggct ttgtctcagg cacttgggat agggattttaa ggagatagag aaagatagga 480
gataggagaa aggagaaaag ggatgtggtta ttggatagaa gggtaatatg gcacctcatc 540

SEQCRF05081156

ccctctttgg	gatgggcatg	ggtgaacaca	gccccaggctt	ttgttctggg	gctggaagag	600
acaggcgaga	gggtctcagc	tgagcatcac	atgaaaggcc	tctgggggat	gggggacctg	660
tgacaggagc	aaggcggggtg	gggtggggatg	ggtgagaggg	tctggaatgt	cccggtgctgc	720
tctgagggag	gagggattggg	agtggagaaa	gaatggggca	tcttatgatt	ctcttgttct	780
ttgtgttgagg	tattcagttgg	gattcattcta	gatctctccc	caagagaatc	aaccagggttt	840
ctgggtacatg	ttagagatggg	agtgaggata	gtctgtgatg	tgcaaaaaat	tctcatgttg	900
accccaagtgc	cccccttctc	tagatccctg	gtctcacaga	ctctctggaa	ctctctcttg	960
atctgacttc	ccctcattcat	gggtgtcattt	caagtcttat	ctcttttacta	tggttctgtat	1020
tgtagtcttgc	aaatatcctg	tctcatatgt	tccaccccaag	gctctttaatc	tgtgtgtgctt	1080
acttttttga	tccagatttt	taaaatcata	agaagacatt	tttatatagt	tcatgaaatt	1140
ttgcatggag	tcgagtttgat	aatttttgtt	agtggtgaatt	aacatttgtgt	ttatttaaga	1200
aaaaaaaata	ttttttttaca	gaaacctact	gaattttagag	gggttttaaaa	taacatgatg	1260
tctgttgattt	gcttttgaat	gcttccagca	aaaaacaacac	gaacaacaaa	aataaaggat	1320
agataaagca	aatgtgacaa	aatgctgata	gttgttggag	cttggggaga	cacatgcaga	1380
gccatcacat	cacttttttt	cagacatctt	tcttggtcag	ttataatcat	tttgtttgtc	1440
cccactccca	atttctactt	gcctcttagtc	catctctctc	actgcttgcc	aaagtgtatc	1500
ttctaaaaa	caaatctgat	catattcaaa	aagcttttga	agggtaagtt	ttatggtata	1560
tgccatatat	cagtacaaca	aaacaaatgc	tctgaggtgc	cggtgacctac	aggataaaat	1620
ccaaactcct	ttgctgggca	ctccaaagccc	ccactctatc	tcttggccct	catctctcat	1680
gagtacatc	agccacattg	ctagtgtctg	ctcattggcct	tctgcttaga	atgtctttatg	1740
ccccagccaa	ctattttactg	tcttcttcag	tcgaccagag	tgcaattttac	ttgtttaaaa	1800
tctatcattt	tggtatatact	ttgtgatgtc	tattatggct	catattaaag	aatgccttgg	1860
attatagtaa	tttatgtata	tgcttatttc	atatacttta	acctgaaccc	cttcagaacc	1920
atttcttttt	catttcttaa	gttcttttga	cctagccagc	tgccgtgtac	gtcgtgggta	1980
ttcagtagat	taaaaatgcac	tttaaggaa	ttcccttgtt	gtccactcaag	tggtctaaggc	2040
tctgtgtctcc	caatgcaggg	gaccaggggt	caatctcagg	tcagggaact	agatcccaac	2100
ggtcacaact	aagaggtttgc	gaagccacaac	tacctgacct	ccaggtccac	aacatctcga	2160
agatccctgc	tgctgcaact	aagtctcagt	gcagtttaaa	atattttttt	aatgcacttt	2220
gaatgtgaga	atgaatgatg	tgctcacagac	actgtttgtcc	cttggaaggg	gaagtgagta	2280
tgattttgag	gccctcatag	tatatcttcc	tttttaggac	ccagagacag	ggagctgcct	2340
gggtgtctcaa	ggcagctcag	aattaaagca	tggaacagac	agctgtatcc	agagtggaca	2400
gaaagccagg	ggcctgactg	ctggagaggt	aggaacttgg	caatttccag	ggaggatatg	2460
gtggaaaatg	gtggggaggg	gaacgggggt	gaatgtactt	aggaagatag	ggagggaaaa	2520
ggcacaacag	gaggagaagc	caaggagcta	attaatgcag	ctgccttttt	caggtggcca	2580
catatccctg	aagggtcagca	atgatggggc	tacactgatt	ggggcaaaat	cttctctctc	2640
tattgtcttg	cactttctcta	aaagccaaaa	gggtctgcca	gatggggcagg	tcacttgggc	2700
caacaacact	atcatcaatg	gtgagtacct	ctccgcccct	ttcccaagggt	ccagaatccc	2760
ttgttatcccc	aatgagctca	aggaatctct	ctctcttttt	tttttttttt	tttttcaaaa	2820
tttatatgtg	aacacataatt	cactgcagaa	aaattagaaa	acacagataa	acccaaaaga	2880
aaaaaaaatta	tagttcccca	aggaagggcac	agaagaccca	gtggacagata	aagtgggata	2940
tcttgggatt	taaaactggtt	accagatagt	gacctgtgac	aagtcactga	attgttttgt	3000
gcttctcatc	ctttatctat	agaaatgggga	tgataaacatt	ttaaaagggtt	cttgttaactg	3060
ttaaaatgtg	ataatatata	aagatttttag	cataatgctc	gccctgtgctg	gtgtcttagta	3120
ccctagtttt	gacgcctttgc	aacccccatg	actgtagccc	accaggctcc	cttgcctcatg	3180
tggtattctgc	agggcaagaat	actggagttg	gtcaccatgc	actctccagc	gggattcttcc	3240
caactcaggg	atcgaaacca	gggtctagcc	tacagtatta	attgatgctg	tattttttac	3300
tttttatccca	ctagctagag	cacatcatcc	tagacatttt	gatacatggc	ctaccaattt	3360
gtgtccagtg	taagaatata	catgtgtgtg	ctcagtgtct	cgatgctgtc	ctagtctttg	3420
caaccctcat	gagctgtagc	ccgcgaaagct	ctctgcacca	tgggattgcc	cagccaagaa	3480
tactggagca	ggttgcattt	tcttctccca	ggggatcttt	caacacaggg	attgtaactt	3540
tgctctctgt	gtttctctga	ttggcagggt	tatttctttac	cactgagcca	ctctgggaaa	3600
cccttaagta	tatacacata	aatcttttat	agtttccatt	ctctcttcta	ccactccaaa	3660
taggttatac	caaggagaat	gtatttttgt	agctaggcag	tattctctga	gccctctctc	3720
gggagctcatg	ttaaagggtt	tgtgtgtacg	tgaggaatgc	cagggtatga	gggagacttg	3780
ctgtcttctt	tctcagggagc	caggtgtggg	gaggacagct	gggtatatccc	caagaacctg	3840
atgataacct	catctctccc	gatggggagc	gctgcccttc	tgggccctcta	cttcagaaaa	3900
gatgctttgt	ttatgtctgg	aagacctggg	gtaagagttt	cccttctctg	gcctgtcat	3960
cacactataa	tctcaacttct	ctcactgatc	cccttcttct	ttgtgtctat	ctctaaattc	4020
tgtaggtttt	cctaactctc	acttccccca	tgactctctc	cttctccaca	gcacttagtc	4080
aaactctatta	tacttcttct	tgggagacct	gctccaatta	tagtcccact	catgtgacc	4140
tctcataagc	acttttttcc	tgcccccaat	atgcaagctt	aaactctctg	aaataaacat	4200
ccttgataag	tctctgacc	ttctctctct	ggttccatct	ctaaccctgc	cccagttctc	4260
tttgaccagt	aacccccctc	cctactcttc	tttccaaaaa	cctcagacca	atactggcaa	4320

SEQCRF05081156

gttctggggg	gccagtgct	tggactgagc	atcgggagac	acaaggcaat	gctgggcaca	4380
tataacatgg	aagtgaactg	ctaccacgcg	cgggggtccc	agagctatgt	gcccctcgct	4440
cactccagtt	cagccttcac	cattactgggt	aaggactgag	gaggggacaa	gcccagttgc	4500
agggcaggag	aaggtgggga	ggctgggctg	gacaggaaag	gggaagaagag	aaatggtgtg	4560
taaccttaca	ggggcagaac	caggaagatg	tgggcagagg	gatgtggggc	ttggagcccg	4620
tgaaggggca	ggcagcttgg	gttggttgaa	aaatatggct	gtgaagaagag	agactgacag	4680
aaagaagaag	ttatggttct	cactttctct	gacctcaatc	ccagaccagg	tggcctttct	4740
gtctgtgtgt	tctcagctgc	aggccttggg	tgggaaggac	aaagccttcc	tgagaagaag	4800
ggctctgagc	tttgccttcc	agctccatga	tcccagtggt	tatttggactg	gggcttggct	4860
ttctctacac	tgggactttg	gtgacagtac	agggaccctg	atctctcggg	cactcacggt	4920
cactcacact	tacctagagt	gtggcccagc	cactgcacag	gtgggtctgc	aggcttgcct	4980
tcctctcacc	tccttgtgct	ctctctcagt	tccaggcact	acagataggg	atgtgacaac	5040
tgacagagct	cttggaaacca	cagctggcca	agtgcctact	acagaagtca	tgggcaccac	5100
acctgtggcag	gtgccaaactg	cagagggccc	tggcaccaca	gttgggtggg	tgcccaaccac	5160
agaggatgta	gttaccacac	ctgagcaggt	ggcaacctcc	aaagtcttaa	gtacacaccc	5220
agtggagatg	ccaactgcaa	aaagtacagg	taggacacct	gaagtgtcaa	ctacagagcc	5280
ctctgtgaacc	acagttacac	agggaacaac	tcagagctg	gtggagacca	cagcttgaga	5340
gggtgtccact	cttgagccctg	cgggttcaaa	tactagctca	ttcatgctca	cagagagttac	5400
tgacagttaag	ggggccacca	tgaatgagtt	ctagagagtg	gggcatgtgt	cacagctctg	5460
aaagactga	agaattgtct	aggaccacga	tgttactcaa	tccttagctt	agcagtgtag	5520
tcctctcaga	atttctcactg	gttttaaac	cccttaagtc	ctctttaatg	gcacagaata	5580
gatccagagt	tcaggaaaac	agggtcttct	cctaggccag	gggtagagag	cttatcttct	5640
cttctctgaag	acgaatttcag	gagcagtggt	gtgatcattt	gtgtgtgtgt	ctcagtgagc	5700
cttgactctt	tgtgacctca	tggactatgg	cccaccaggc	tcctctgtcc	atagaattct	5760
ccaggtcaaga	actgtggagt	gggtggccat	ttcttcttcc	aggggatttt	cctgcccag	5820
ggattaaacc	cgaattggca	gggtgattct	ttaccggagc	cacctagaaa	gtcccatgtg	5880
atcattagat	aatacttata	ctctattttc	tgattaagtg	taaacacaga	aatctttctg	5940
acaccacttc	ccaccctctg	attccccatc	caaagttagt	ttacctggaa	tgtgtgtagg	6000
aataactaaa	agggagaagt	gagatagtga	cactatgact	taacactgtc	caatgtgctt	6060
accagggacc	tggcacagtg	taggggttga	taaacatttg	ggaatgtctaa	aatcttgact	6120
ctaacctctg	gactctgggg	cagtcatttc	tcttggccct	ttctttatct	taaaaaatga	6180
gagtttccag	ctcttgtctg	attctaagcc	tggactcagt	agctctgact	ctacctggaa	6240
aaatgcttgt	tgggctctgt	ttcaggttag	tcatttgctt	tttgactttg	ctctcttaat	6300
ctctctcttc	aggctccctg	agtcctctgc	cggatgacac	tgccacctta	gtccttgaga	6360
agcgccaagg	ccccctggat	tgtgttctgt	atcgctatgg	ctctcttttc	ctcaccctgg	6420
acaattgtctg	tgagctttgc	ctacattgtc	gtaagcttgg	tggaggaggg	cgtgtgtctg	6480
ttagggttgg	ccagttggag	cacaccttgg	aaagaaattac	tcacctggac	aaggagaata	6540
ccagatctcc	aggggttttca	tatgaaggca	gaatgggatt	agggaggcag	cccaggaacc	6600
ttctctggcca	tgggctcttg	gggagggtaa	gtagaggagt	ctcagactta	aaaaaatctt	6660
gcaactttgc	agagggattt	agatctctaca	agatctctaca	ggctgtgtca	tcctagtgaag	6720
gagatgcatt	tgagctgact	gtgtcttgcc	aaggcgggtg	agtgctccac	gggtgtccctg	6780
agaactctctg	gggtgactgc	tgtctctgtc	tctgtgtctt	agtgctccctt	cccagatctc	6840
ctgacgtaa	ctgacatctc	tcccaggcta	cccaaggga	ctgtcatgga	catctcatcg	6900
ccagggtgtg	agctgcctgc	ccagcgctg	ttctagcctg	tgccccccag	cccagcctcg	6960
cagctgggtt	tgaccagggt	actgaagggt	ggctcaggga	cttactgctt	caatgtgtct	7020
ttggctgtgt	ccaatagctc	ggcgatggtc	agcaccacga	gtgtcatgcg	tggttaggtag	7080
ttgggacaaga	ggttaggtga	agacaggggg	agatggtaga	ggttaacctac	tagaggaagc	7140
agacactgaa	tgacagccga	tcctggattc	caccataagg	gcaaggaagca	ggccttgaat	7200
aggctctctc	gtctctgggg	atcttctgtg	tgctaacagc	tttgttgctt	gcactcttga	7260
tatacaggtg	agatccccgc	catctctctc	ccactctttt	accccttatt	accaccacca	7320
ctcttctcaga	tgggaagaag	aaaccaccaa	cccttttggg	aaagtgtaga	gtcccaagaaa	7380
gagccctacac	ttgggaagtt	aacaggtcta	ggctgcagtc	ttgtgtgtgtg	gacctctggg	7440
aagtcctafca	acccttctga	gccactgaaa	agttaggaac	ataataacctg	ctctgtgggg	7500
ctgttttctg	ggctctagac	aatgtgagta	aaacacctgg	ttctgaaccta	taagttggaat	7560
aaatgatgat	ctcaatgact	gtgtgtatga	ataatatcaa	cagtgagagca	gaactcagtg	7620
aactgagttc	tcacactgct	agaaaaggcaa	atccctaggg	ctggaggagct	gaggtctcca	7680
aagcagggaa	gctctgtagg	tgagaggggaa	atggtcagag	cttaccataat	acataagaga	7740
ggataaacc	tgttggtag	agaaggaggg	agccaggatc	aagaccaaagt	aacctgggtt	7800
tatgtgttag	tctttttttt	ttatagaagc	acaaaggagt	tgcatttgac	caccactaac	7860
gcttttctct	gcttttcttc	caatatcagc	cgaagactta	tgaagcaagg	ctcagctagc	7920
ccccctcccc	agctgccaca	cggtagaacc	cagtggttac	gtctgccctg	ggtcttccgc	7980
tcttgcccca	ttggtgagag	caaacctctc	ctcagtgga	agcaggtctg	agtgtctcta	8040
tgtagagta	tgatttacc	aggtggacag	caaggcctgt	cttttctctg	gtcttccctc	8100

agagactacc attgcctgaa ataaagactc agaacttg

8138

<210> 15
 <211> 2086
 <212> DNA
 <213> artificial sequence

<220>
 <223> Charolais SILVER

<400> 15
 ggtctttggt tgctggaagg aagaacagga tggatctggt gctgagaaaa taccttctcc 60
 atgtggctct gatgggtggt ctcttgctg taaggaccac agaaggaccc agagacaggg 120
 actggcttgg tgctcaagg cagctcagaa ttaagcatg gaacagacag ctgtatccag 180
 agtggacaga aagccagggg cctgactgct ggagaggtag ccacatatcc ctgaaggtag 240
 gcaatgatgg gctacactg attggggcaa atgtctctct ctctattgcc ttgcactttc 300
 ctaaaagcca aaaggtgctg ccagatgggc aggtcatctg ggccaacaac accatcatca 360
 atgggagcca ggtgtgggga ggacagctgg tatatcccca agaacctgat gatacctgca 420
 tcttcccccga tggggagccc tgccttctg gccctctatc tcagaaaaga tgccttgttt 480
 atgtctgtaa gacctgggac caatactggc aagttctggg gggcccagtg tctggactga 540
 gcatcgggac agacaaggca atgctgggca catataacat ggaagtgaact gtctaccacc 600
 gccgggggtc ccagagctat gtgcccctcg ctcactccag ttcagccttc accattactg 660
 accaggtgcc ctctcttgtg agtgtgtctc agctgcaggg cttggatgga aggaacaagc 720
 gcttctgagc aaagcagcct ctgaccttgg ccctccagct ccatgatccc agtggctatt 780
 tggctggggc tgacctttcc tacacctggg actttgttga cagtacaggg accctgatct 840
 ctcgggcact caccgttact cacacttacc tagagtctgg cccagtcact gcacaggtgg 900
 tgcctgagcg tgccattctc ctcaactcct gtggctctct tccagttcca ggcactacag 960
 ataggactgt gacaactgca gaggctcctg gaaccacagc tggccaaagt cctactacag 1020
 aagtcatggg caccacacct ggcaggtgac caactgcaga ggcctctggc accacagttg 1080
 ggtgggtgct aaccacagag gatgtaggta ccacacctga gcaggtggca accctcaaa 1140
 tcttaagtac aacaccagtg gagatgcca ctgcaaaagc tacaggtagg acacctgaag 1200
 tgtaactac agagccctct ggaaccacag ttacacaggg aacaactcca gagctggtag 1260
 agaccacag tggagaggtg tccactctgt agcctgcggg ttcaaatcct agctcattca 1320
 tgctacaga aggtactgca ggcctccctga gtcccctgcc ggaatgacat gccaccttag 1380
 tctctggagaa gcgccaagcc cccctggatt gtgttctgta tgcctatggc tctctttccc 1440
 tcaccttga catgttccag ggtattgaga gtgtgtagat cctacaggct gtgtcatcca 1500
 gtgaaggaga tgcatttgag ctgacttgtt ctgtccaagg cgggctacc aaggaagcct 1560
 gcatggacat ctcatgcgca ggggtgtcagc tgcctgccca gcggcttgt cagcctgtgc 1620
 cccccagccc agcctggcag ctggttttgc accaggtagc gaagggtggc tcagggacct 1680
 actgcctcaa ttgttctttg gctgatgcc aagcctggc gatgtctcag acccagctgt 1740
 tcatgcttgg gcaagaagca ggcctcaggc gttctgtggc atcttctgtg 1800
 tgctaacagc ttgtgtgctt gcatctctga tatacaggcg aagacttagt aagcaaggtt 1860
 cagcagctcc ctttcccagc ctgccacacg gtgagaccca gtggctacgt ctgcccttgg 1920
 tcttctcttc ttgccccatt ggtgagagca aacccctcct cagtgagacg caggtctgag 1980
 tgctcttatt tgaagtcatg atttaccagc gtggacagca aggcctgtct tttctctggg 2040
 ctctccctcag agactaccat tgcctgaaat aaagactcag aacttg 2086

<210> 16
 <211> 1584
 <212> DNA
 <213> artificial sequence

<220>
 <223> RPE1

<400> 16
 ccaatactgg caagttctgg gggggccagt gtctggactg agcatcggga cagacaaggc 60
 aatgctgggc acatataaca tggaaagtac tgtctaccac gccggggggt ccagagagcta 120
 tgtgccccct gctcactcca gtctcagcctt caccattact gaccagggtg cctttcttgt 180
 gagtgtgtct cagctgcagg ctttggatgg aaggaacaag cgcttcttga gaaagcagcc 240
 tctgaccttt gccctccagc tccatgatcc cagtggtatc ttggctgggg tgacactttc 300

SEQCRF05081156

ctacacctgg	gactttgggtg	acagttacagg	gacctggtac	tctcggggcac	tcacgggtcac	360
tcacacctta	ctagagtcttg	gccaggtcac	tgccaggttg	gtgtgtgcagg	ctgcccattcc	420
tctcaccttc	tggtggctcct	ctccagttcc	aggcactaca	gataggcatg	tgacaactgc	480
agaggctcct	ggaaccacag	ctggccaagt	gcttactaca	gaagtcatgg	gcaccacacc	540
tggccagggtg	ccaactgcag	aggccccctgg	caccacagtt	gggtgggtgc	caaccacaga	600
ggatgtagggt	accacacctg	agcaggtggc	aacctccaaa	gtcttaagta	caaccacagt	660
ggagatgccca	actgcaaaaag	ctacaggttag	gacacctgaa	gtgtcaacta	caagagccctc	720
tggaaaccaca	gtttacacagg	gaacaactcc	agagctgggtg	gagaccacag	ctggagaggtg	780
gtccactcct	gagcctgctgg	gttcaaatac	tagctcattc	atgctctacag	aaggtactgc	840
aggtcctcctg	agtcctcctgc	cggatgacac	tgccacctta	gtcctggaga	agcgccaagc	900
ccccctggat	tgtgttctgt	atcgctatgg	ctccttttcc	ctcaccctgg	caattgtcag	960
tattgagagt	gctgagatcc	tacaggtgtg	gtcatccagt	gaaggagatg	catttgagct	1020
gactgtgtct	tgccaaggcg	ggctacccaa	ggaagcctgc	atggacatct	catcgccagg	1080
gtgtcagctg	cttgccaccag	ggctgtgtca	gcctgtgccc	cccagcccag	cctgcccagct	1140
ggttttgcac	caggtactga	aggggtggctc	agggacctac	tgccctcaatg	tgtctttggc	1200
tgatgccaat	agcctggcga	tggtcagcac	ccagctgtgc	atgcctgggc	aagaagcagg	1260
cttcaggcag	gtcctctctg	tcgtgggcat	cttgctgggtg	ctaacagctt	tgttgcttgc	1320
atctctgata	tacaggcgaa	gacttatgaa	gcaagggtca	gcagtcctccc	ttccccagct	1380
gccacacggt	agaaccacgt	ggctacgtct	gccctgggtc	ttccgctctt	gccccattgg	1440
tgagagcaaa	ccccctctca	gtggacagca	ggtctgagtg	ctcttatgtg	aagtcattgat	1500
ttaccaggtg	ggacagcaag	gccgtctctt	tctctggctt	tcctccagag	actaccattg	1560
cttgaataaa	agactcagaa	cttg				1584

<210> 17

<211> 649

<212> PRT

<213> Charolais SILVER

<400> 17

Met Asp Leu Val Leu Arg Lys Tyr Leu Leu His Val Ala Leu Met Gly
1 5 10 15

Val Leu Leu Ala Val Arg Thr Thr Glu Gly Pro Arg Asp Arg Asp Trp
20 25 30

Leu Gly Val Ser Arg Gln Leu Arg Ile Lys Ala Trp Asn Arg Gln Leu
35 40 45

Tyr Pro Glu Trp Thr Glu Ser Gln Gly Pro Asp Cys Trp Arg Gly Gly
50 55 60

His Ile Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
65 70 75 80

Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Lys Ser Gln Lys Val
85 90 95

Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly
100 105 110

Ser Gln Val Trp Gly Gly Gln Leu Val Tyr Pro Gln Glu Pro Asp Asp
115 120 125

SEQCRF05081156

Thr Cys Ile Phe Pro Asp Gly Glu Pro Cys Pro Ser Gly Pro Leu Ser
130 135 140

Gln Lys Arg Cys Phe Val Tyr Val Trp Lys Thr Trp Asp Gln Tyr Trp
145 150 155 160

Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Asp Lys
165 170 175

Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr His Arg Arg
180 185 190

Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr
195 200 205

Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala
210 215 220

Leu Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro Leu Thr Phe
225 230 235 240

Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Gly Ala Asp Leu
245 250 255

Ser Tyr Thr Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu Ile Ser Arg
260 265 270

Ala Leu Thr Val Thr His Thr Tyr Leu Glu Ser Gly Pro Val Thr Ala
275 280 285

Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser
290 295 300

Pro Val Pro Gly Thr Thr Asp Arg His Val Thr Thr Ala Glu Ala Pro
305 310 315 320

Gly Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Met Gly Thr Thr
325 330 335

Pro Gly Gln Val Pro Thr Ala Glu Ala Pro Gly Thr Thr Val Gly Trp
340 345 350

Val Pro Thr Thr Glu Asp Val Gly Thr Thr Pro Glu Gln Val Ala Thr
355 360 365

Ser Lys Val Leu Ser Thr Thr Pro Val Glu Met Pro Thr Ala Lys Ala
370 375 380

SEQCRF05081156

Thr Gly Arg Thr Pro Glu Val Ser Thr Thr Glu Pro Ser Gly Thr Thr
 385 390 395 400
 Val Thr Gln Gly Thr Thr Pro Glu Leu Val Glu Thr Thr Ala Gly Glu
 405 410 415
 Val Ser Thr Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser Phe Met Pro
 420 425 430
 Thr Glu Gly Thr Ala Gly Ser Leu Ser Pro Leu Pro Asp Asp Thr Ala
 435 440 445
 Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys Val Leu Tyr
 450 455 460
 Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val Gln Gly Ile Glu
 465 470 475 480
 Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly Asp Ala Phe
 485 490 495
 Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met
 500 505 510
 Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu Cys Gln
 515 520 525
 Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Val Leu
 530 535 540
 Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala
 545 550 555 560
 Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly Gln Glu
 565 570 575
 Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu Val Leu
 580 585 590
 Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys
 595 600 605
 Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg Thr Gln
 610 615 620
 Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly Glu Ser
 Page 35

625

630

635

640

Lys Pro Leu Leu Ser Gly Gln Gln Val
645

<210> 18
<211> 491
<212> PRT
<213> RPE1

<400> 18

Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly
1 5 10 15

Thr Asp Lys Ala Met Leu Gly Thr Tyr Asn Met Glu Val Thr Val Tyr
20 25 30

His Arg Arg Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ser Ser Ser
35 40 45

Ala Phe Thr Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln
50 55 60

Leu Gln Ala Leu Asp Gly Arg Asn Lys Arg Phe Leu Arg Lys Gln Pro
65 70 75 80

Leu Thr Phe Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Gly
85 90 95

Ala Asp Leu Ser Tyr Thr Trp Asp Phe Gly Asp Ser Thr Gly Thr Leu
100 105 110

Ile Ser Arg Ala Leu Thr Val Thr His Thr Tyr Leu Glu Ser Gly Pro
115 120 125

Val Thr Ala Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys
130 135 140

Gly Ser Ser Pro Val Pro Gly Thr Thr Asp Arg His Val Thr Thr Ala
145 150 155 160

Glu Ala Pro Gly Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Met
165 170 175

Gly Thr Thr Pro Gly Gln Val Pro Thr Ala Glu Ala Pro Gly Thr Thr
180 185 190

Val Gly Trp Val Pro Thr Thr Glu Asp Val Gly Thr Thr Pro Glu Gln
Page 36

195

200

Val Ala Thr Ser Lys Val Leu Ser Thr Thr Pro Val Glu Met Pro Thr
210 215

Ala Lys Ala Thr Gly Arg Thr Pro Glu Val Ser Thr Thr Glu Pro Ser
225 230 235 240

Gly Thr Thr Val Thr Gln Gly Thr Thr Pro Glu Leu Val Glu Thr Thr
245 250 255

Ala Gly Glu Val Ser Thr Pro Glu Pro Ala Gly Ser Asn Thr Ser Ser
260 265 270

Phe Met Pro Thr Glu Gly Thr Ala Gly Ser Leu Ser Pro Leu Pro Asp
275 280 285

Asp Thr Ala Thr Leu Val Leu Glu Lys Arg Gln Ala Pro Leu Asp Cys
290 295 300

Val Leu Tyr Arg Tyr Gly Ser Phe Ser Leu Thr Leu Asp Ile Val Ser
305 310 315 320

Ile Glu Ser Ala Glu Ile Leu Gln Ala Val Ser Ser Ser Glu Gly Asp
325 330 335

Ala Phe Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala
340 345 350

Cys Met Asp Ile Ser Ser Pro Gly Cys Gln Leu Pro Ala Gln Arg Leu
355 360 365

Cys Gln Pro Val Pro Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln
370 375 380

Val Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala
385 390 395 400

Asp Ala Asn Ser Leu Ala Met Val Ser Thr Gln Leu Val Met Pro Gly
405 410 415

Gln Glu Ala Gly Leu Arg Gln Ala Pro Leu Phe Val Gly Ile Leu Leu
420 425 430

Val Leu Thr Ala Leu Leu Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu
435 440 445

SEQCRF05081156

Met Lys Gln Gly Ser Ala Val Pro Leu Pro Gln Leu Pro His Gly Arg
 450 455 460

Thr Gln Trp Leu Arg Leu Pro Trp Val Phe Arg Ser Cys Pro Ile Gly
 465 470 475 480

Glu Ser Lys Pro Leu Leu Ser Gly Gln Gln Val
 485 490